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**FIG. 1**

<i>Bet v 1</i> sense	5' - AATTATGAGACTGAGACCACCTCTGTTATCCCAGCAGCTCG	-3'
<i>Bet v 1</i> non-sense	3' - TTAATACTCTGACTCTGGTGGAGACAATAGGGTCGTCGAGC	-5'
sense primer	5' - TGAGACCCCTCTGTTATCCCAG	-3'
non-sense primer	3' - ATACTCTGACTCTGGGGGAGACA	-5'

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FIG. 2

all	sense	1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGTCTCAGTCTCATA
2	sense	4: 186Bv, 31-mer 5'-GATACCCTCTTTCCACAGGTGCACCCCAAG
2	non-sense	5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA
3	sense	6: 188Bv, 23-mer 5'-AACATTTTCAGGAAATGGAGGGCC
3	non-sense	7: 189Bv, 23-mer 5'-TTTCTGAAATGTTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTTCCCGAA
4	non-sense	9: 191Bv, 23-mer 5'-AGCTGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer 5'-GGACCATGCAAACCTTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTTGATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer 5'-TTTCCCTCAGGCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCCTGGAAC
7	non-sense	15: 197Bv, 24-mer 5'-CCCTCCAGATCCTTCAATGTTTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTGTGATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCAGTTGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

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FIG. 3

1 (A-C)

GGTGTGTTTAAATTATGAGACTGAGACCACCTCTGTTATCCCAGCAGCTCGACTGTTCAAG 60
 G V F N Y E T E T T-P S V I P A A R L F K 20

9 (A-G) 2 (A-C) 2 (A-C)

GCCTTTATCCTTGATGGCGATAACCTCTTTCCAAAGGTTGCACCCCAAGCCATTAGCAGT 120
 A F I L D-G G D N-T L F P K-Q V A P Q A I S S 40

3 (GA-TC) 7 (AA-TC) 4 (G-C) 6 (GA-TC)

GTTGAAAACATTGAAGGAAATGGAGGGCCTGGAACCATTAAAGAAGATCAGCTTTCCCGAA 180
 V E N I E-S G N-S G G P G T I K K-N I S F P E-S 60

5 (CA-TG)

GGCCTCCCTTTCAAGTACGTGAAGGACAGAGTTGATGAGGTGGACCACACAACTTCAAA 240
 G L P F K Y V K D R V D E V D H T-A N F K 80

TACAATTACAGCGTGATCGAGGGCGGTCCCATAGGCGACACATTGGAGAAGATCTCCAAC 300
 Y N Y S V I E G G P I G D T L E K I S N 100

10 (GAG-CAC) 8 (CCC-TGG)

GAGATAAAGATAGTGGCAACCCTGATGGAGGATCCATCTTGAAGATCAGCAACAAGTAC 360
 E I K I V A T P-G D G G S I L K I S N K Y 120

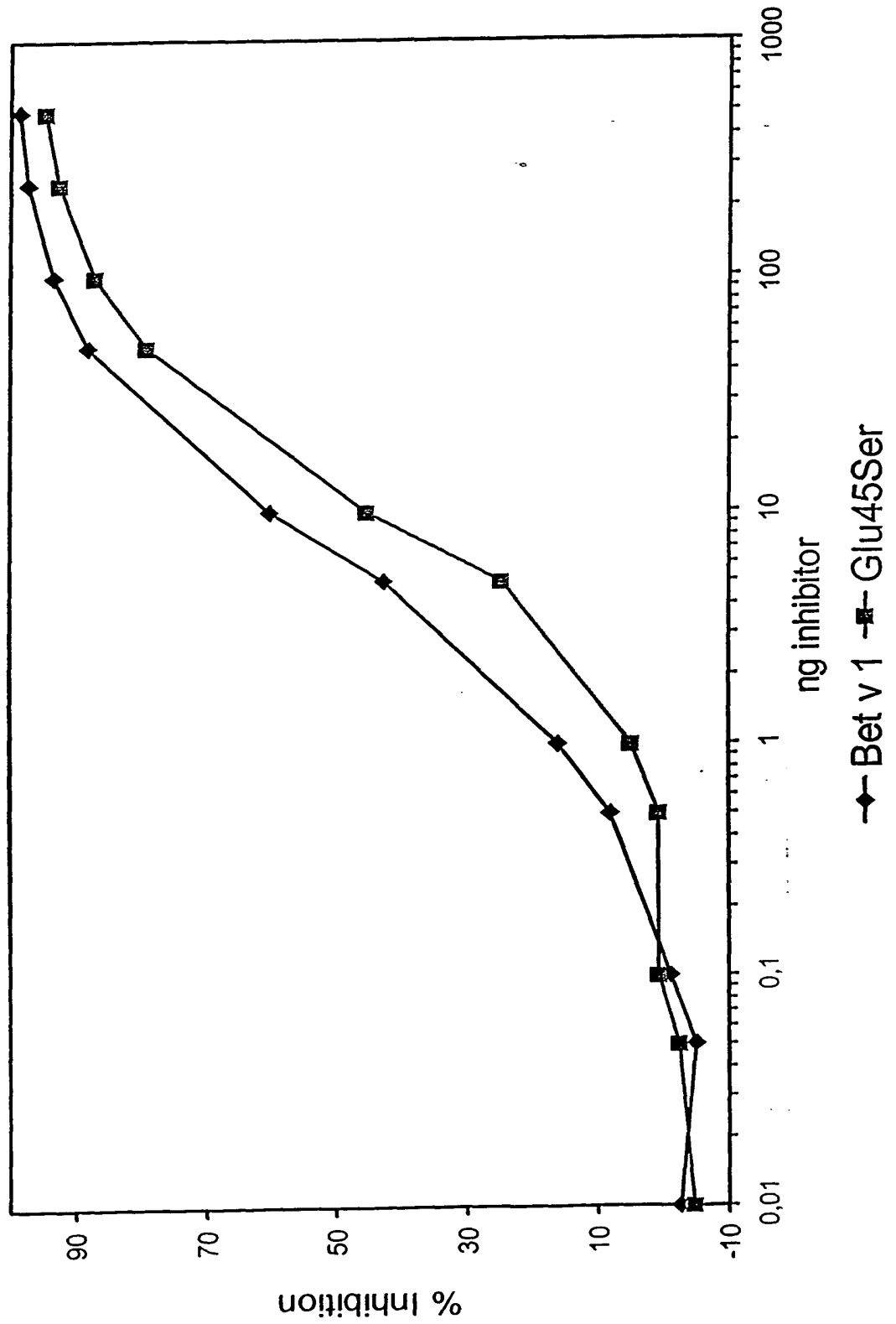
CACACCAAAGGTGACCATGAGGTGAAGGCAGAGCAGGTTAAGGCAAGTAAAGAAATGGGC 420
 H T K G D H E V K A E Q V K A S K E M G 140

GAGACACTTTTGAGGGCCGTTGAGAGCTACCTCTTGGCACACTCCGATGCCTACAATAA 480
 E T L L R A V E S Y L L A H S D A Y N stop 159

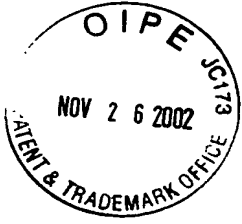
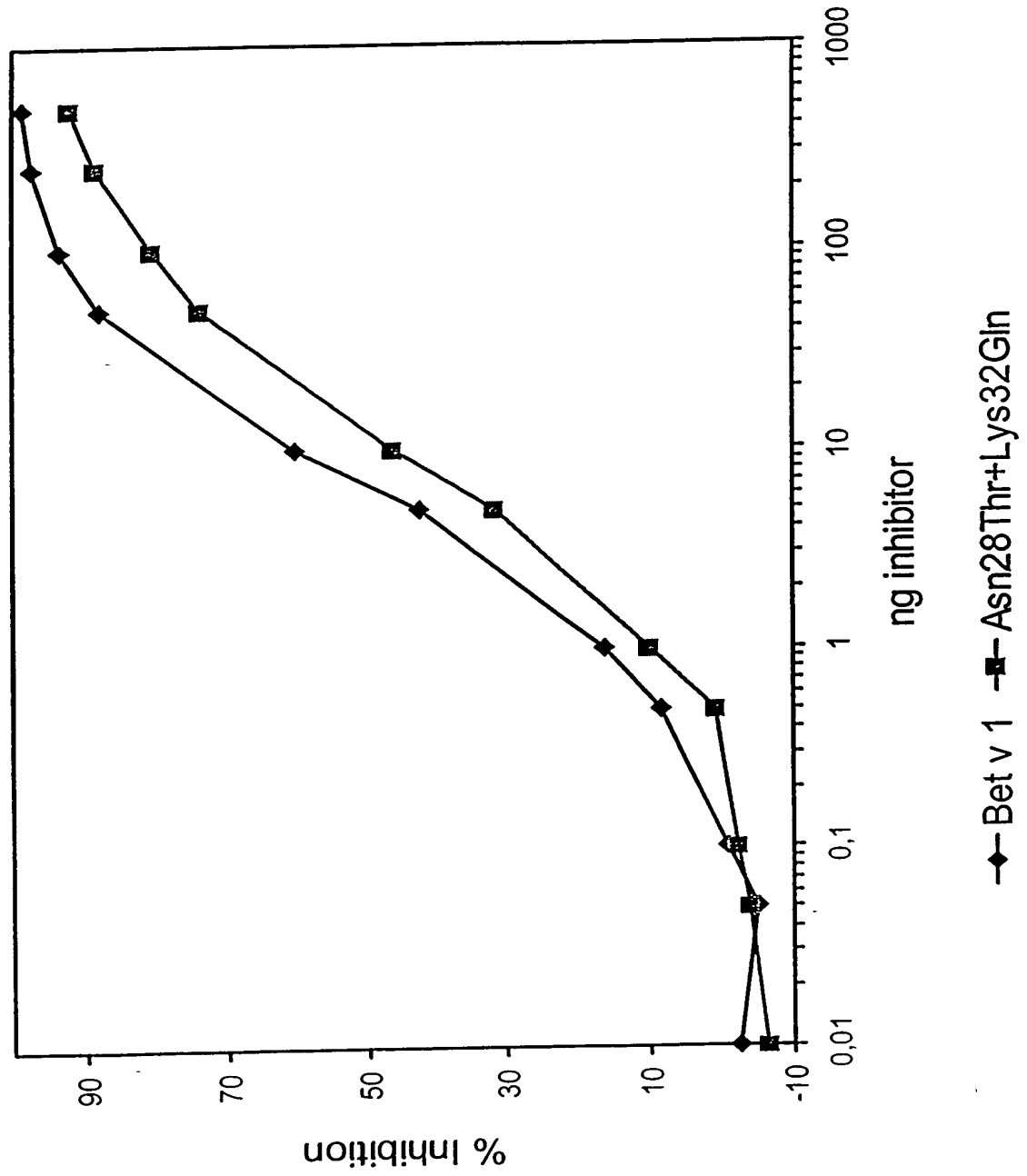
10/001,245



FIG. 4



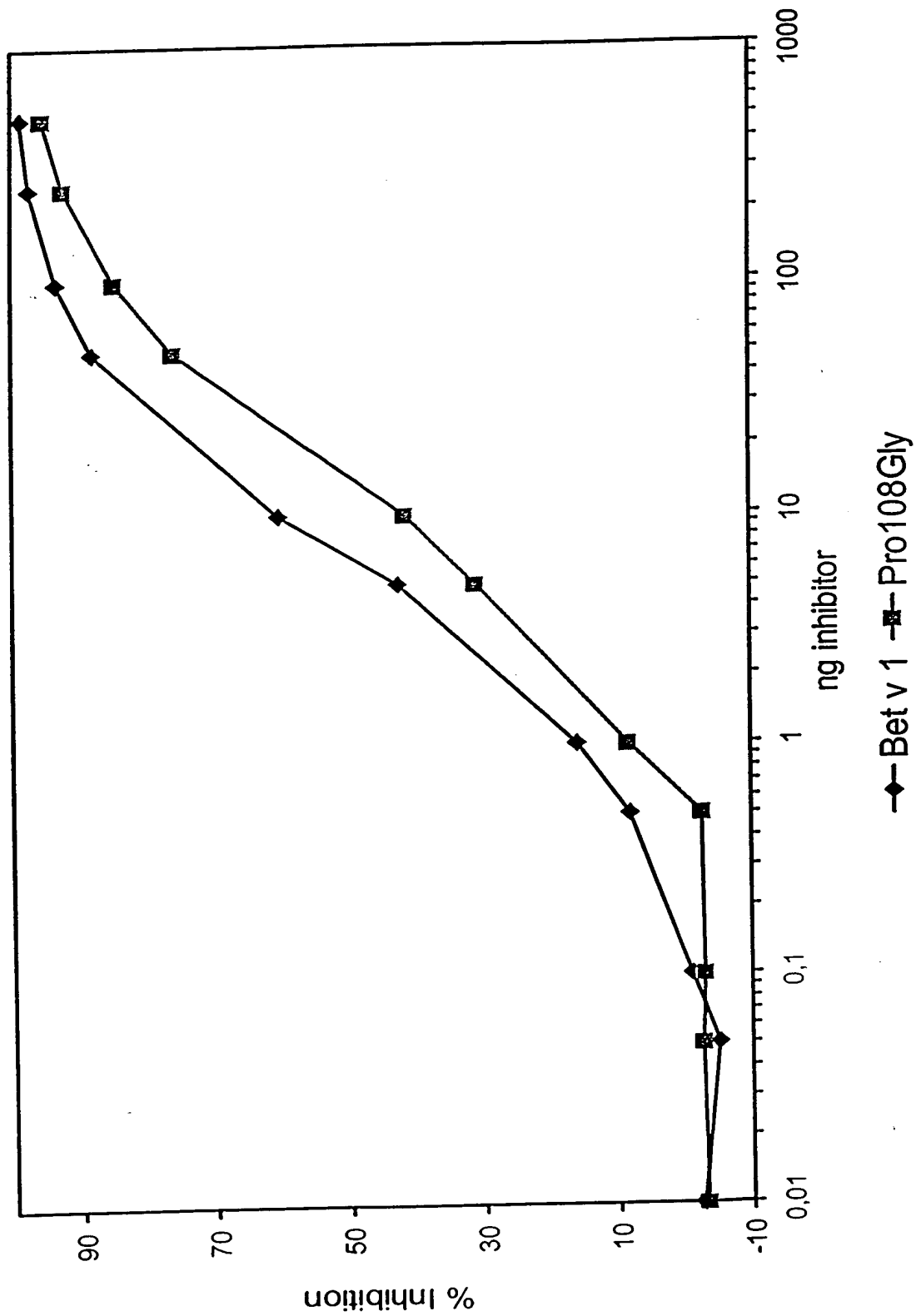
10/001,245

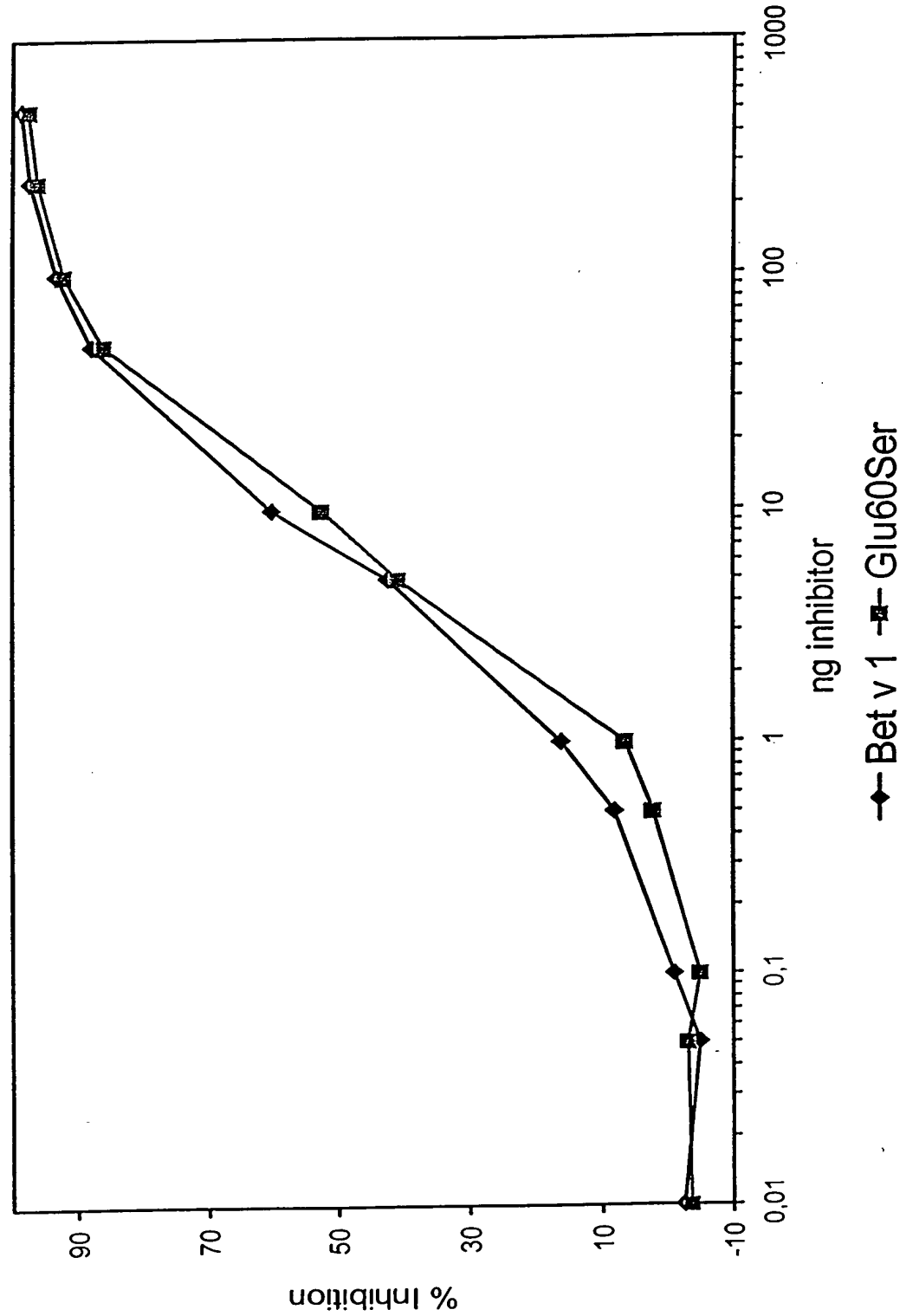
**FIG. 5**

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FIG. 6



**FIG. 7**

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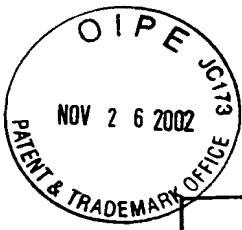
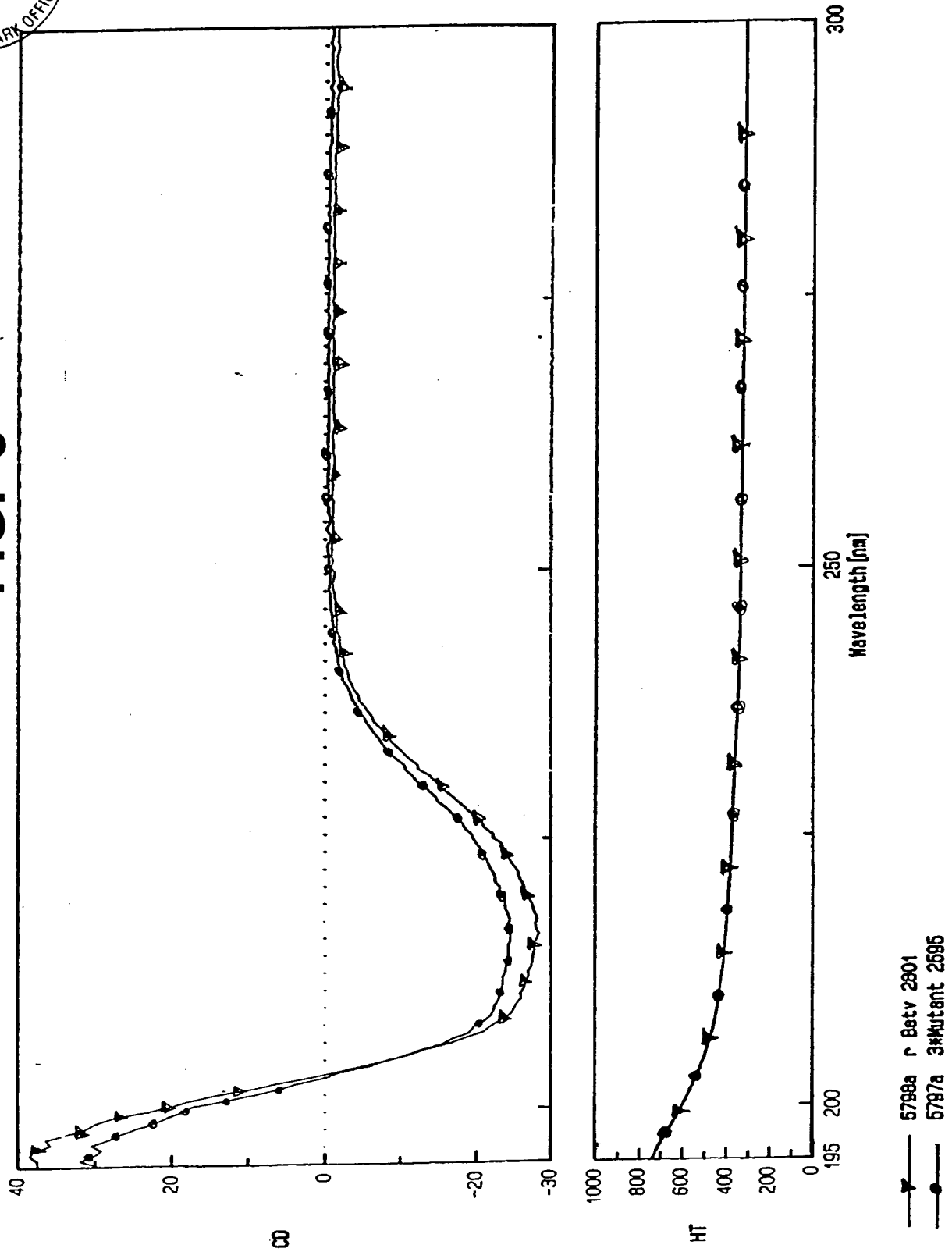
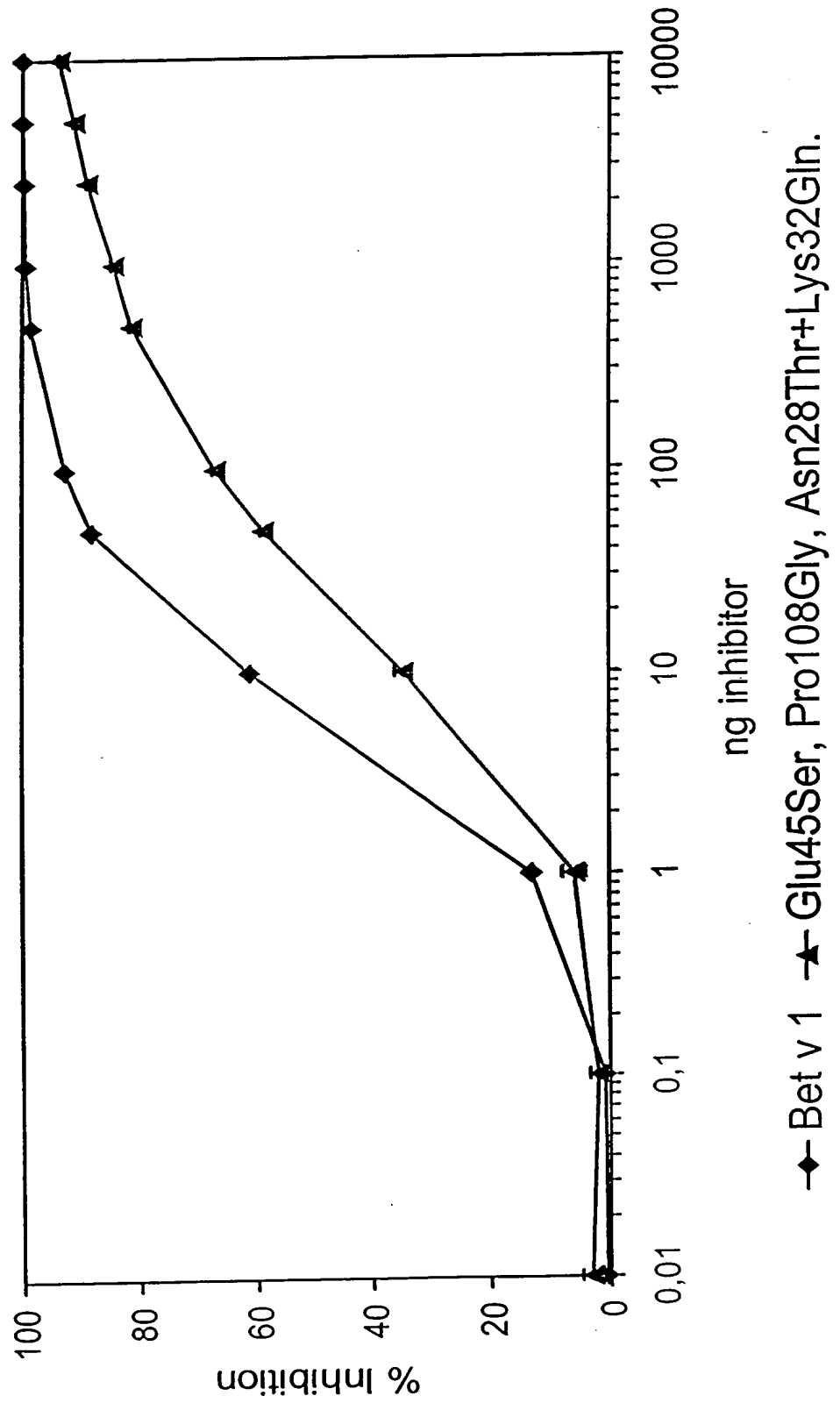


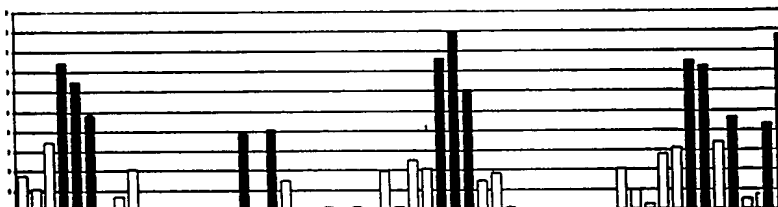
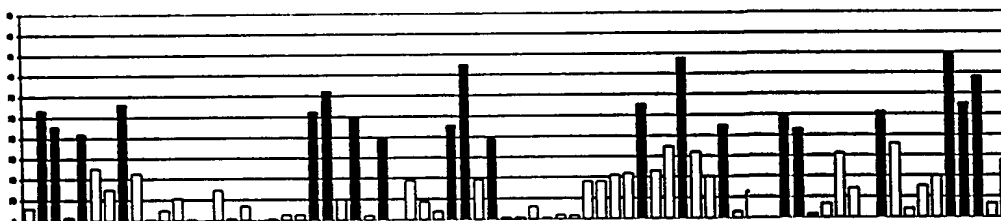
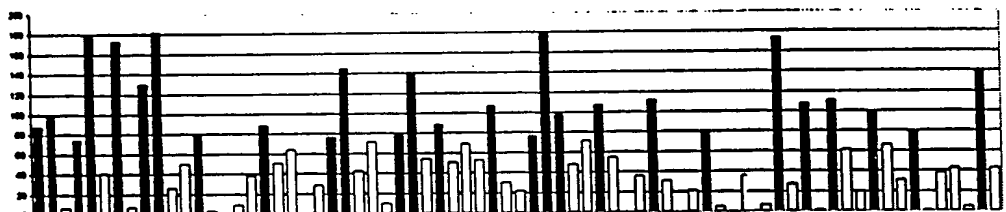
FIG. 8



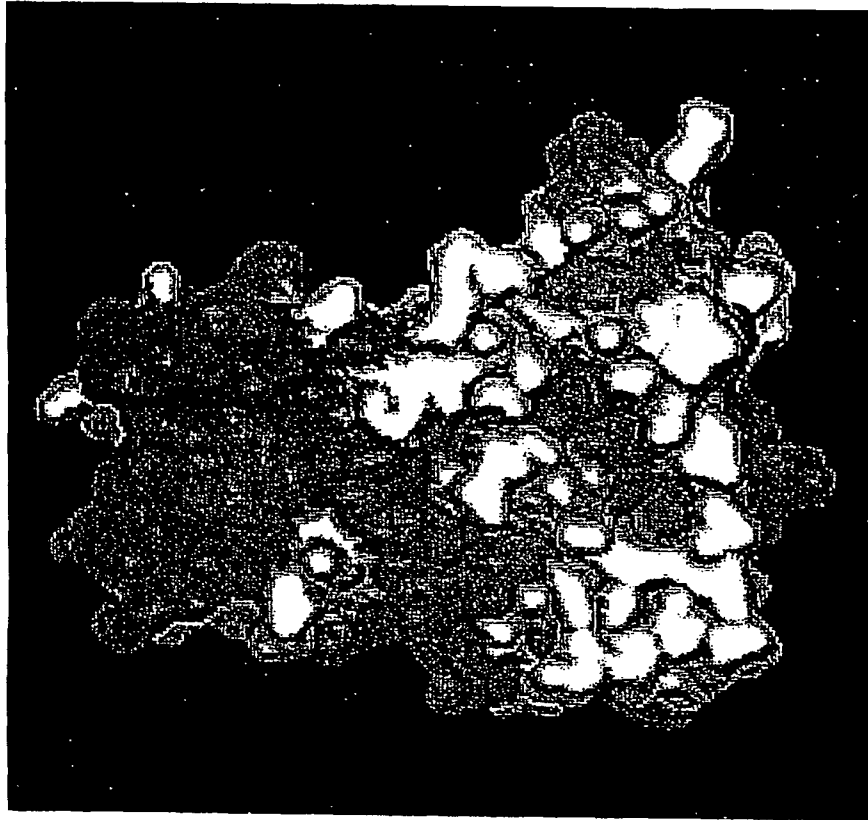
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**FIG. 9**

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**FIG. 10 A**

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**FIG. 10 B**

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FIG. 11 A

Ves v 5 mutant 1 (K72A)

Ves v 5 sense	5'-	ACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGA	-3'
Ves v 5 non-sense	3'-	TGGTGTCTCGGAGGTCGCTTCTTATACTTTTAAACCATACCT	-5'
sense primer	5'-	CCAGCGGCTAATATGAAAAAT	-3'
non-sense primer	3'-	GTCGGAGGTCGCGATTATAC	-5'

FIG. 11 B

Ves v 5 mutant 2 (Y96A)

Ves v 5 sense	5'-	GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG	-3'
Ves v 5 non-sense	3'-	CCGATTAGTTACAGTTATACCAAGTGCTATGAACGTCCCTAC	-5'
sense primer	5'-	TGTCAAGCTGGTCACGATACT	-3'
non-sense primer	3'-	TTAGTTACAGTTCCGACCAAGTG	-5'

FIG. 12

all sense 1: XhoI start, 38-mer:

EcoRI
 5'-CCGCTCGAGAAAAGAAACAATTATTGTAAAAATAAAATG
 L E K R N N Y C K I K
 Kex2 cleavage site amino terminus of Ves v 5

1 sense	1: K72As	21-mer	5'-CCAGCGGCTAATATGAAAAAT
1 non-sense	2: K72Aa	21-mer	5'-CATATTAGCCGCTGGAGGCTG
2 sense	3: Y96As	21-mer	5'-TGTCAAGCTGGTCACGATACT
2 non-sense	4: Y96Aa	21-mer	5'-GTGACCAGCTTGACATTGATT
all non-sense	7: CT-pPICZαA,	21-mer	5'-ATTCATCAGCTGCGAGATAGG

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FIG. 13

1	AACAATTATTGTAAAATAAAATGTTTGAAAGGAGGTGTCCATACTGCCTGCAAATATGGA	60
1	N N Y C K I K C L K G G V H T A C K Y G	20
61	AGTCTTAAACCGAATTGCGGTAATAAGGTAGTGGTATCCTATGGTCTAACGAAACAAGAG	120
21	S L K P N C G N K V V V S Y G L T K Q E	40
121	AAACAAGACATCTTAAAGGAGCACAATGACTTTAGACAAAAAATTGCACGAGGATTGGAG	180
41	K Q D I L K E H N D F R Q K I A R G L E	60
	1 [K72A] (AAG-GCT)	
181	ACTAGAGGTAATCCTGGACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGAAC	240
61	T R G N P G P Q P P A K N M K N L V W N	80
	2 [Y96A] (TA-GC)	
241	GACGAGTTAGCTTATGTGCGCCCAAGTGTGGGCTAATCAATGTCAATATGGTCACGATACT	300
81	D E L A Y V A Q V W A N Q C Q Y G H D T	100
301	TGCAGGGATGTAGCAAAATATCAGGTTGGACAAAACGTAGCCTTAACAGGTAGCACGGCT	360
101	C R D V A K Y Q V G Q N V A L T G S T A	120
361	GCTAAATACGATGATCCAGTTAAACTAGTTAAAATGTGGGAAGATGAAGTGAAAGATTAT	420
121	A K Y D D P V K L V K M W E D E V K D Y	140
421	AATCCTAAGAAAAAGTTTTCGGGAAACGACTTTCTGAAAACCGGCCATTACACTCAAATG	480
141	N P K K K F S G N D F L K T G H Y T Q M	160
481	GTTTGGGCTAACACCAAGGAAGTTGGTTGTGGAAGTATAAAATACATTCAAGAGAAATGG	540
161	V W A N T K E V G C G S I K Y I Q E K W	180
541	CACAAACATTACCTTGATGTGAATTATGGACCCAGCGGAAACTTTAAGAATGAGGAACTT	600
181	H K H Y L V C N Y G P S G N F K N E E L	200
601	TATCAAACAAAGTAA	612
201	Y Q T K stop	204

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FIG. 14

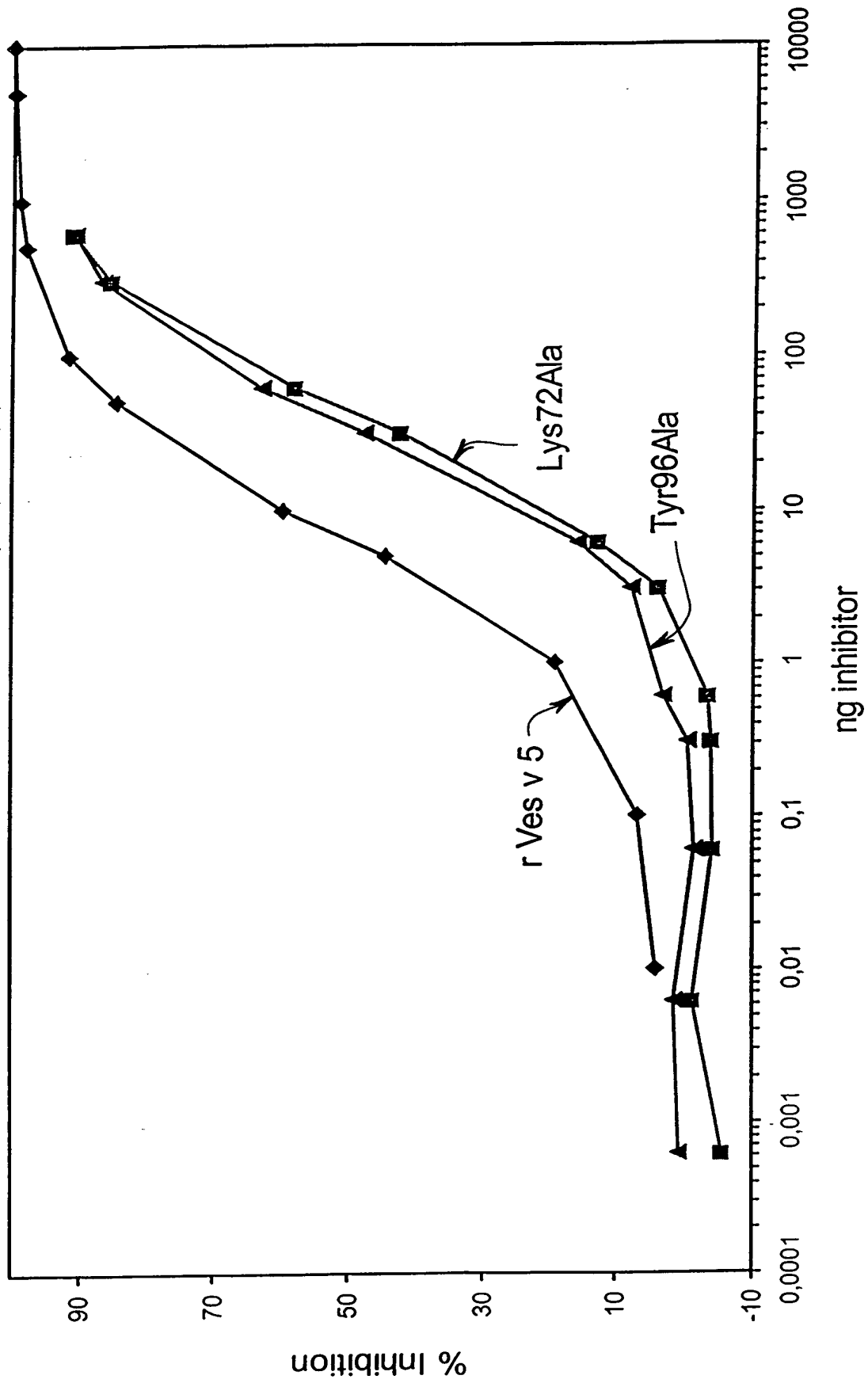
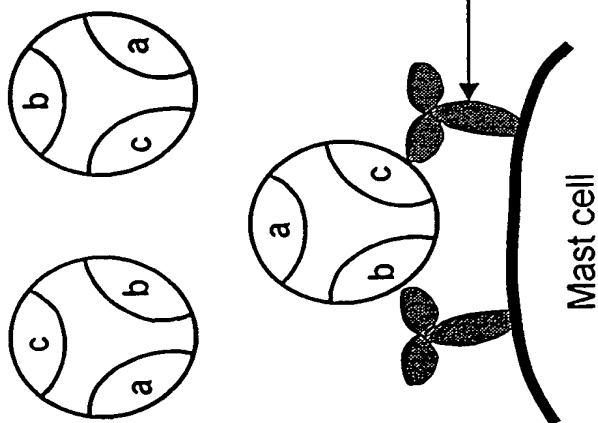


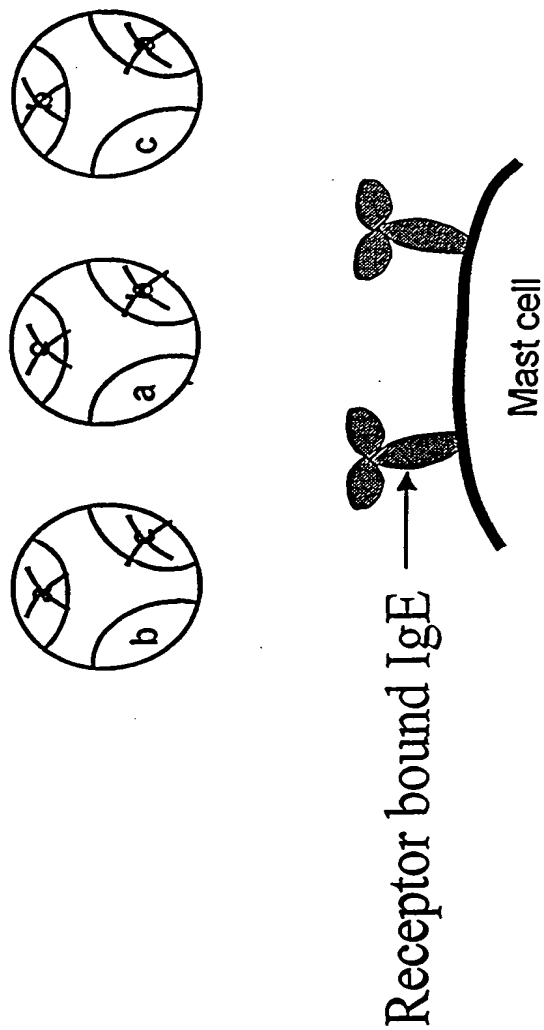


FIG. 15 A



Cross-linking

FIG. 15B



No cross-linking

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FIG. 16 A

DNA SEQUENCE

ORIGIN

```

1      cacaaattct tctttctcc ttactactga tcattaatct gaaaacaaaa ccaaacaac
61     cattcaaaat gatgtacaaa attttgtgtc ttcatgtgt ggtcgcagcc gttgctcgtg
121    atcaagtcga tgtcaaagat tgtgccaatc atgaaatcaa aaaagtttg gtaccaggat
181    gccatgggtc agaaccatgt atcattcatc gtggtaaacc attccaattg gaagccggtt
241    tcgaagccaa ccaaaacaca aaaacggcta aaattgaaat caaagcctca atcgatgggt
301    tagaagttga tgttcccggt atcgatccaa atgcatgcc a ttacatgaaa tgcccatgg
361    ttaaaggaca acaatatgat attaaatata catggaatgt tccgaaaatt gcacccaaat
421    ctgaaaatgt tgcgtcact gttaaagtta tgggtgatga tgggtgttg gcctgtgcta
481    ttgctactca tgctaaaatc cgcgattaaa tcaaacaaaa ttattgatt ttgtaatcac
541    aatgattga ttttcttcc aaaaaaaaaa taaataaaat ttgggaatt c

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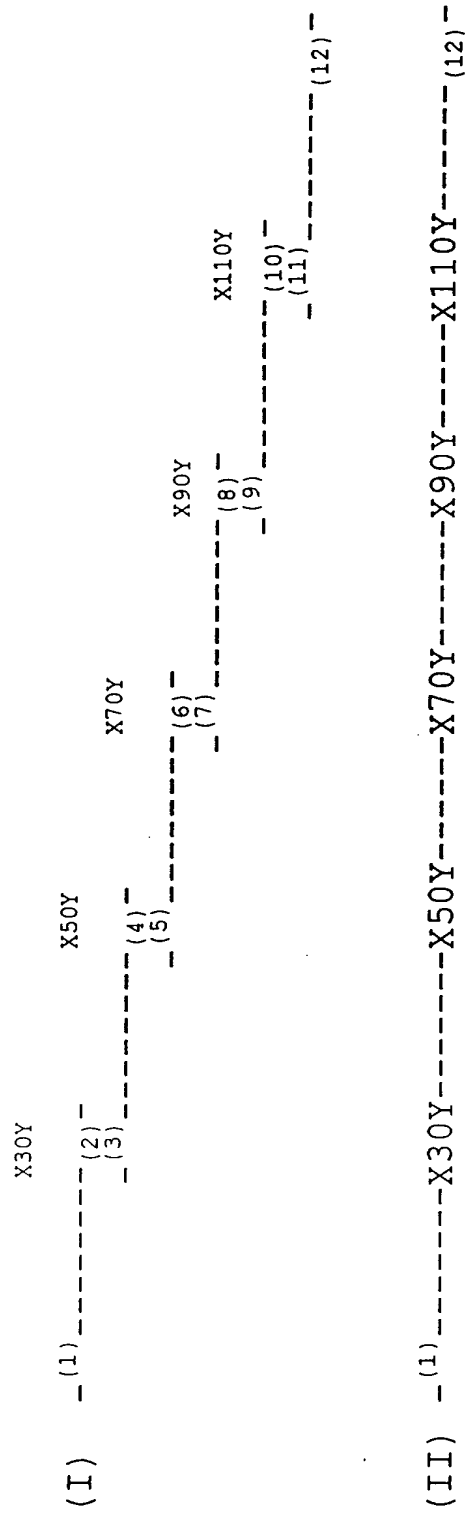
FIG. 16 B

```

1      mmykilclsl lvaavardqv dvkdcanhei kkvlvpgchg sepciihrk pfqleavfea
61     nqntktakie ikasidglev dvpgidpnac hymkcplvkg qqydikytwn vpkiapksen
121    vvvtkvmgd dgvlacaiat hakird

```


FIG. 17



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FIG. 18 A

DNA template: Bet v 1 (2589) carrying the Y5V mutation.

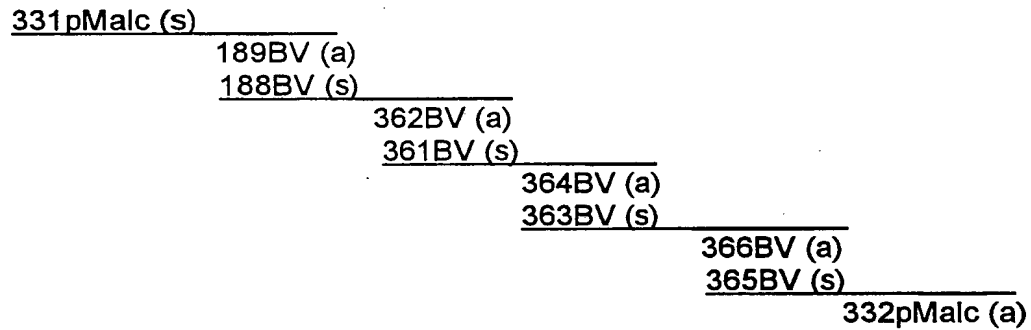
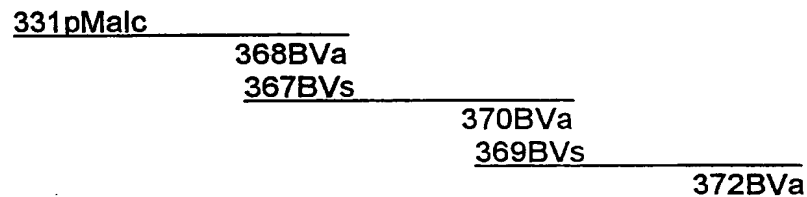


FIG. 18 B

DNA template: Bet v 1 (2571) carrying N28T, K32Q, P108G mutations.

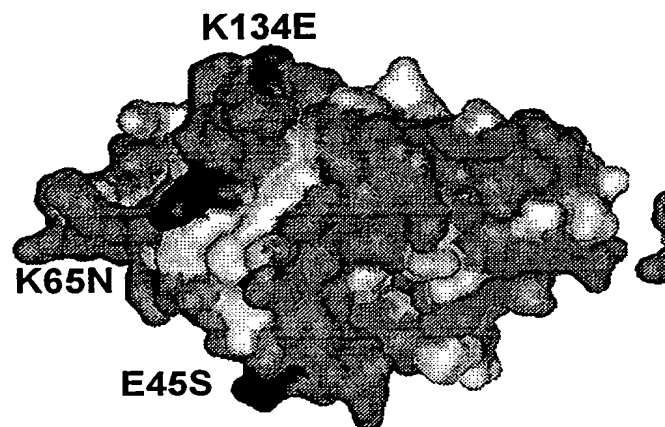
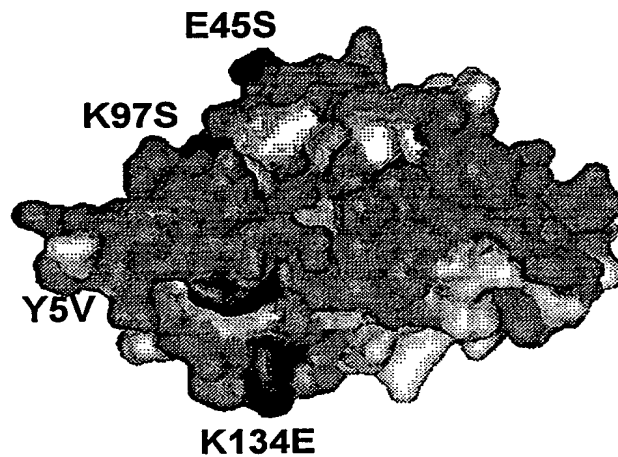
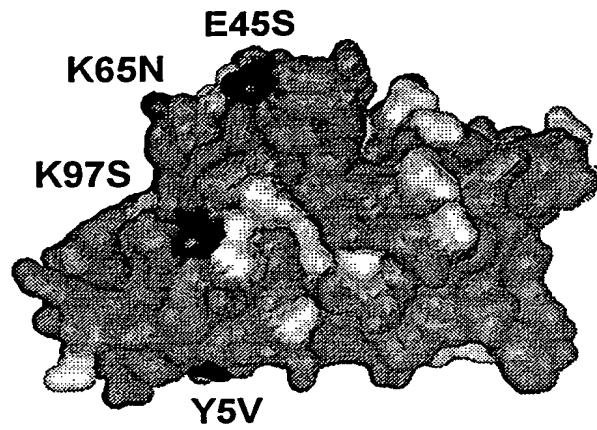


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FIG. 19 A

Bet v 1 (2628)

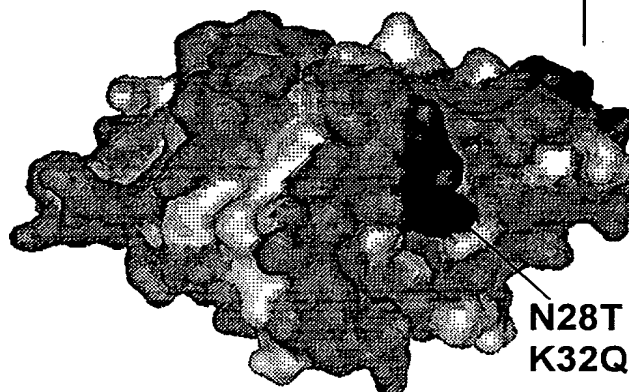
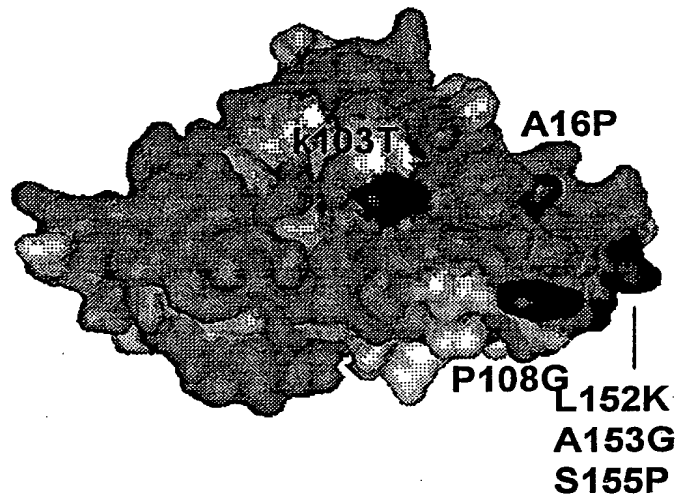
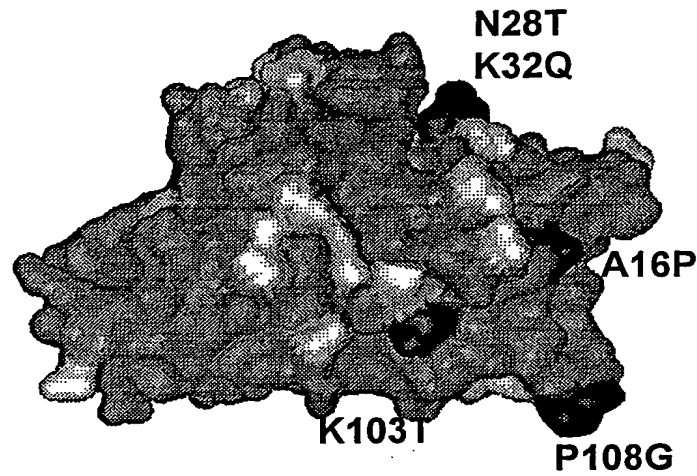


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FIG. 19 B

Bet v 1 (2637)



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FIG. 20

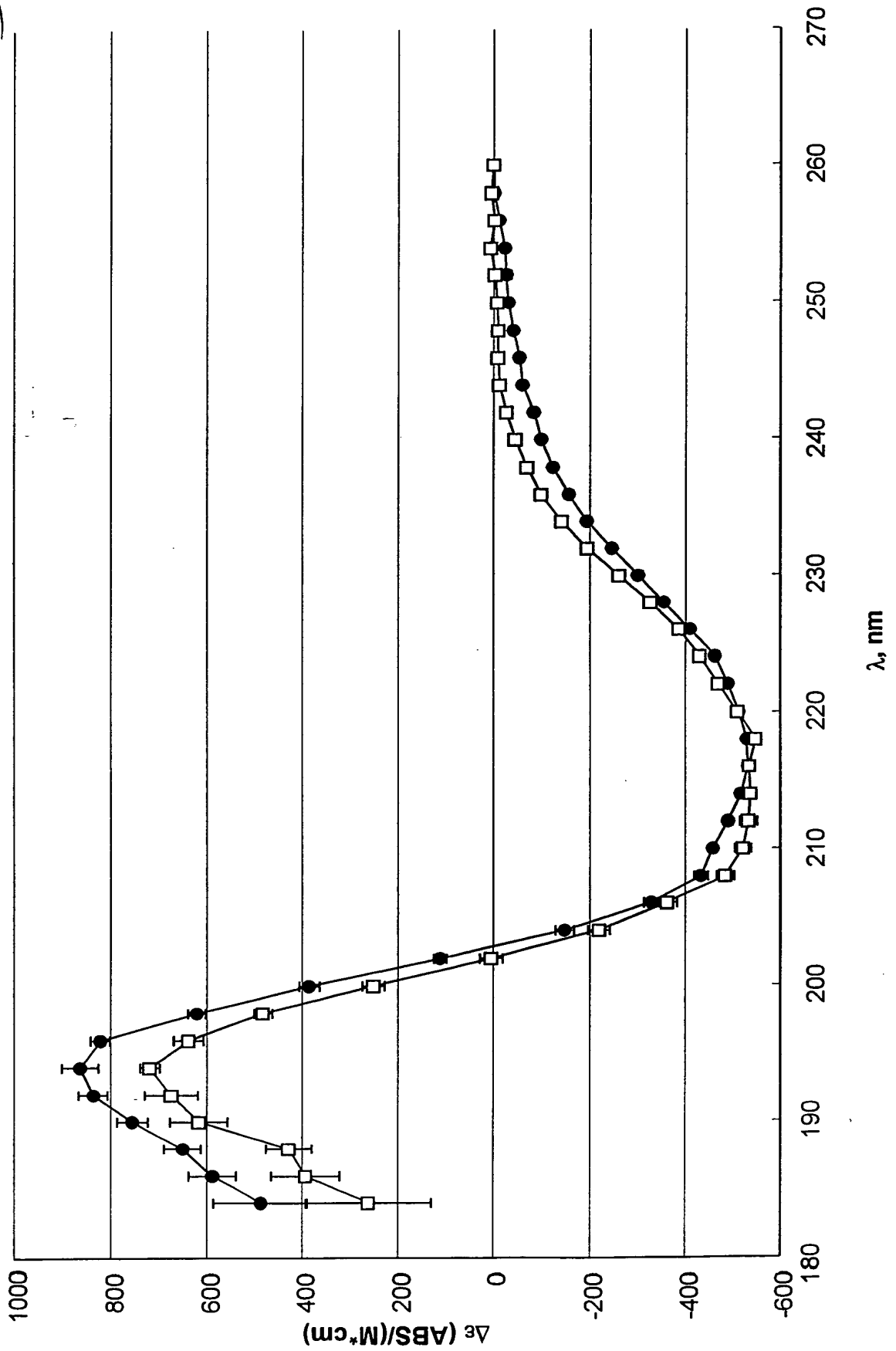
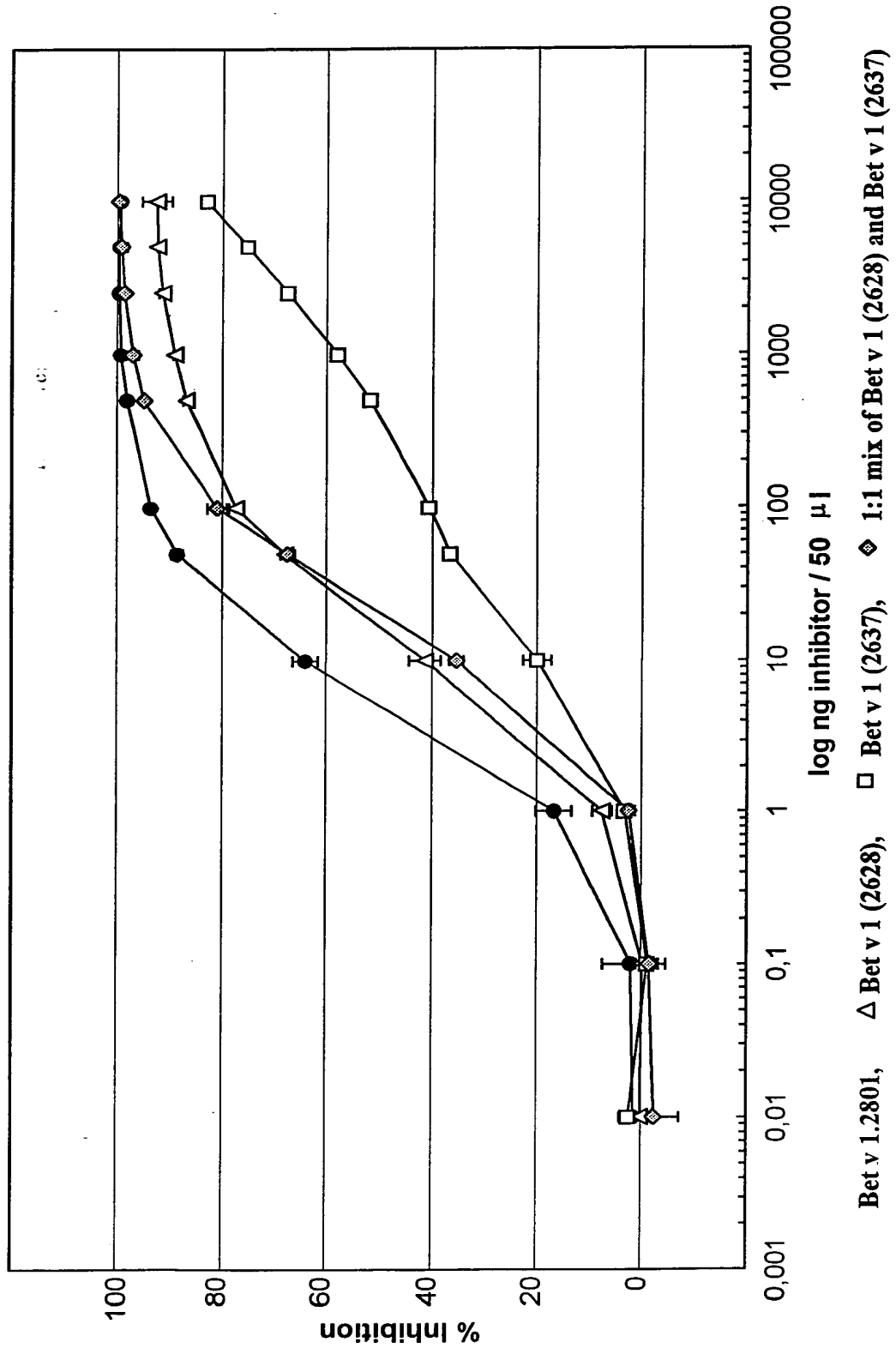




FIG. 21



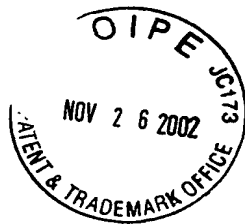


FIG. 22

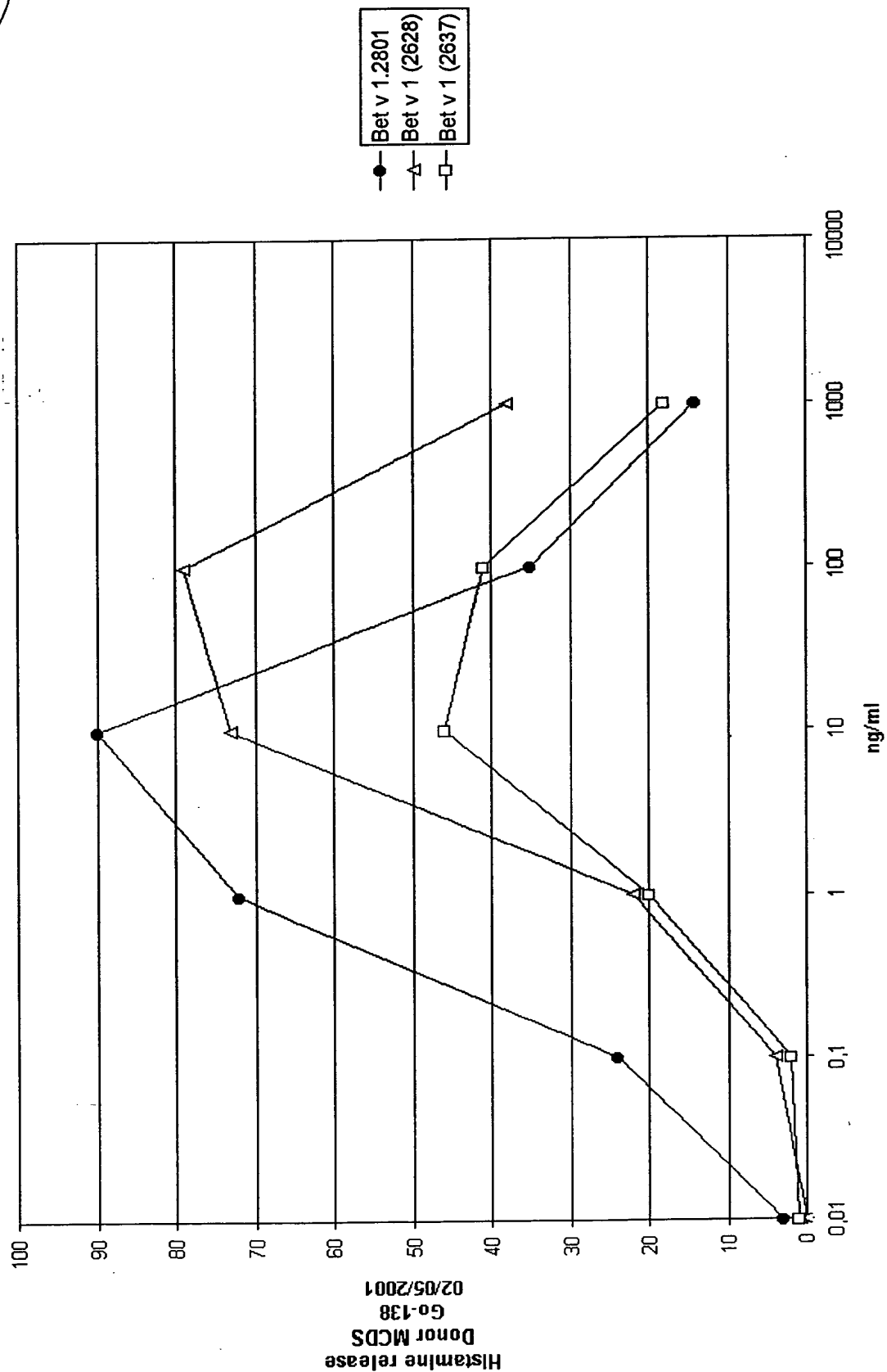


FIG. 23

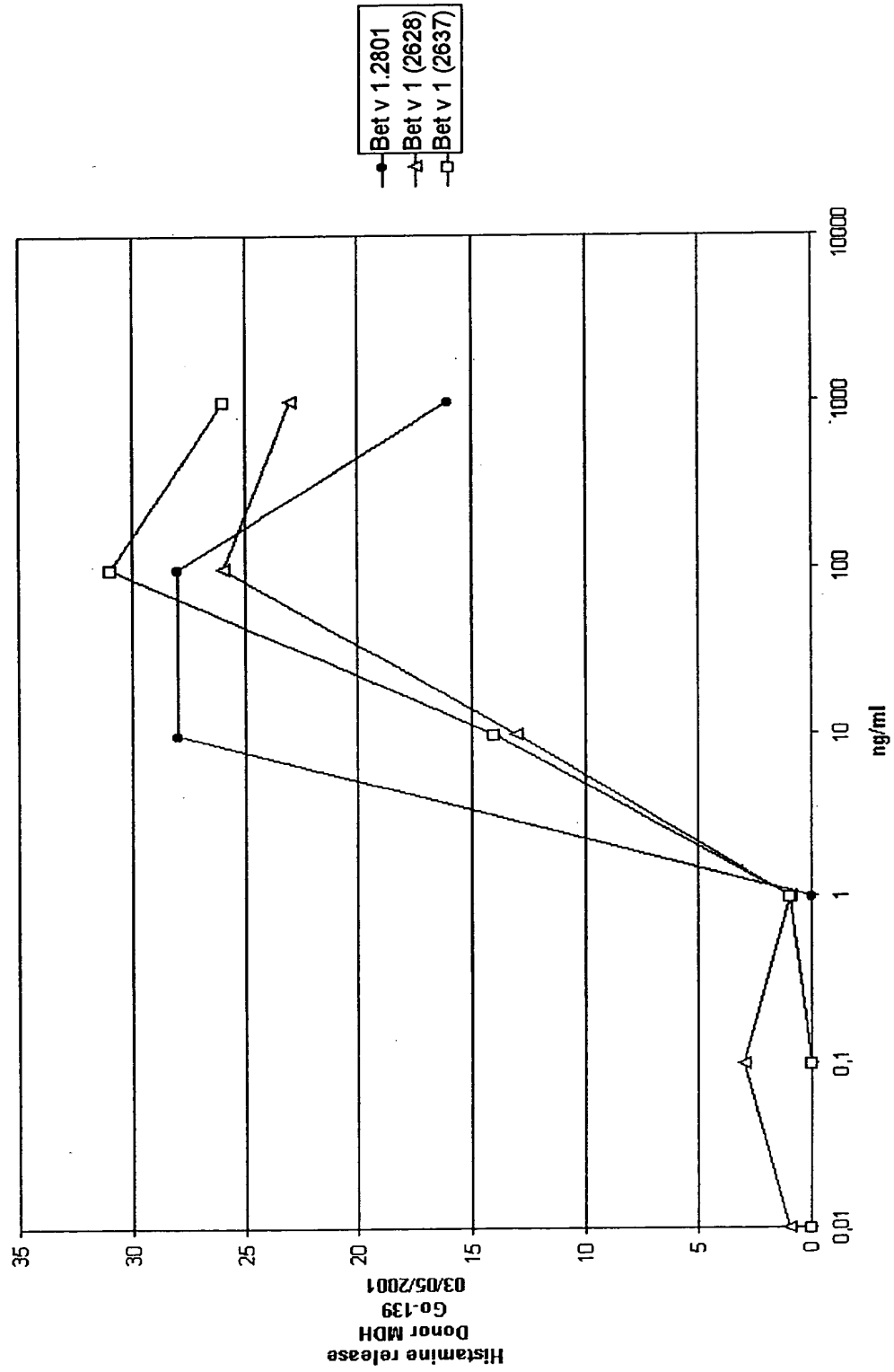
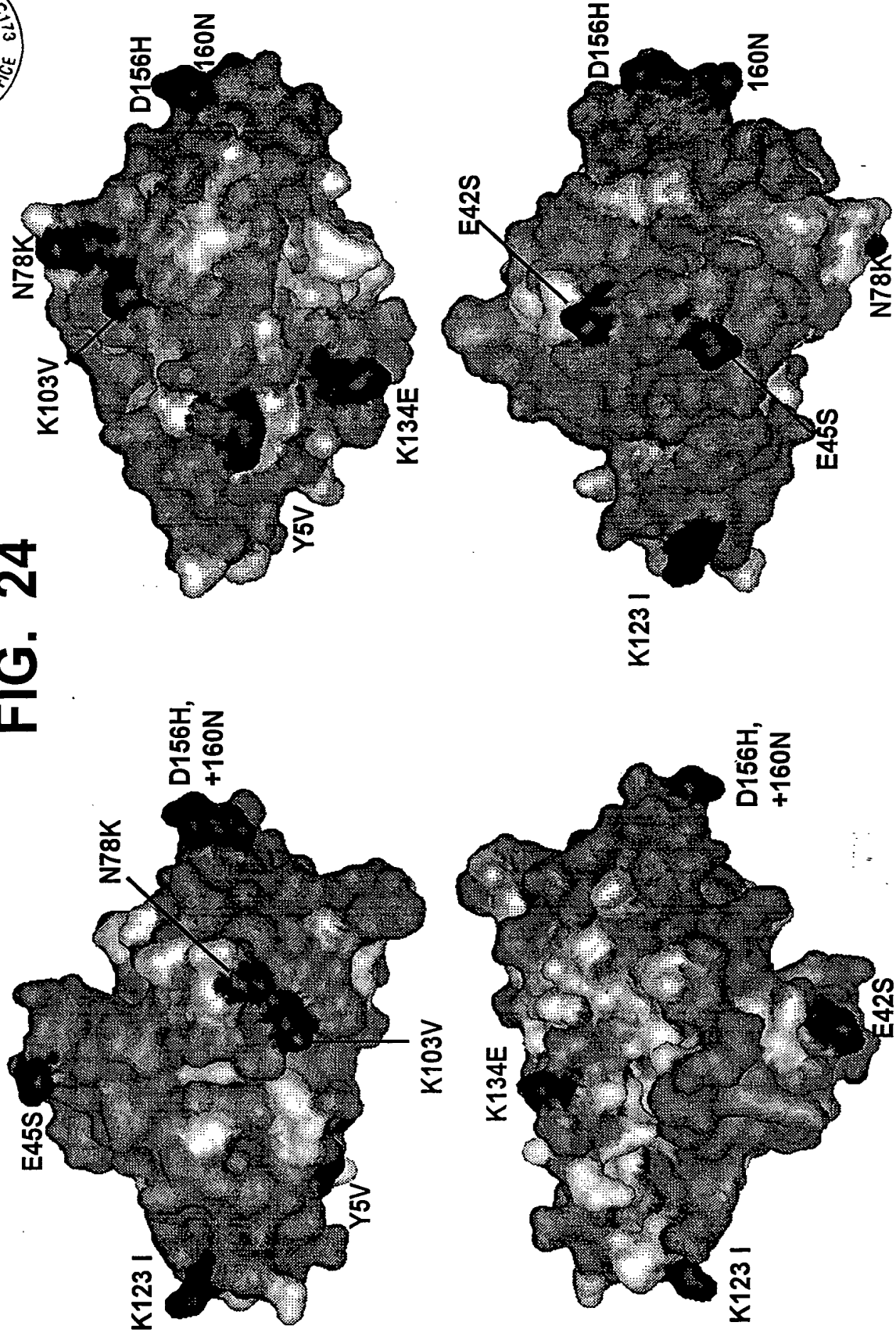


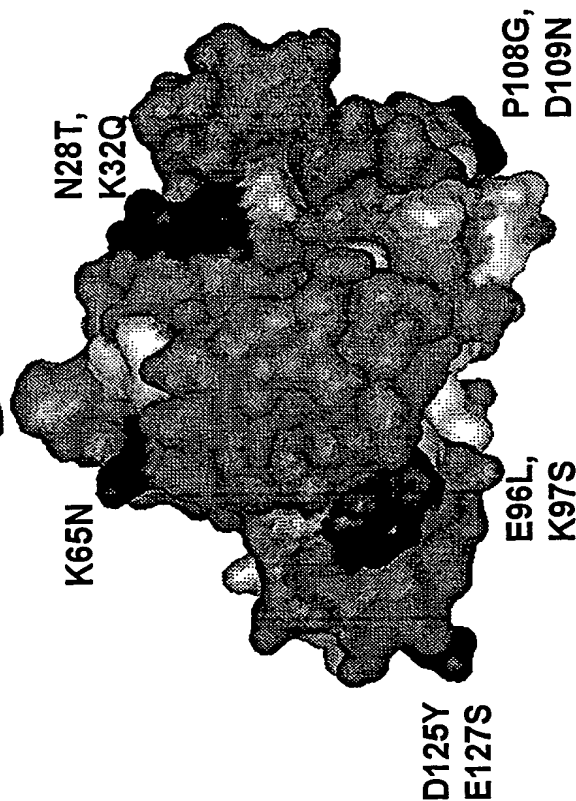
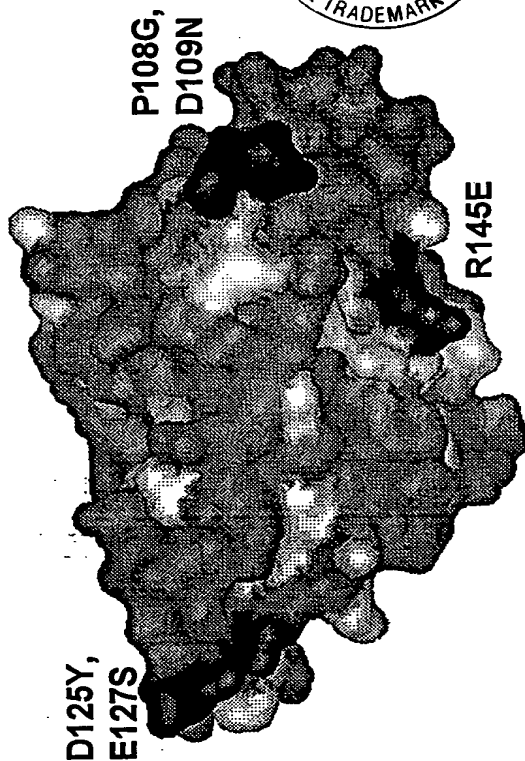
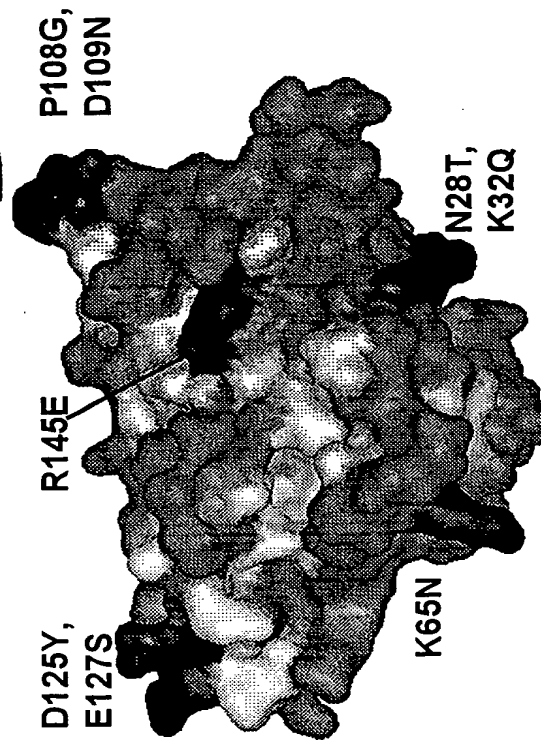
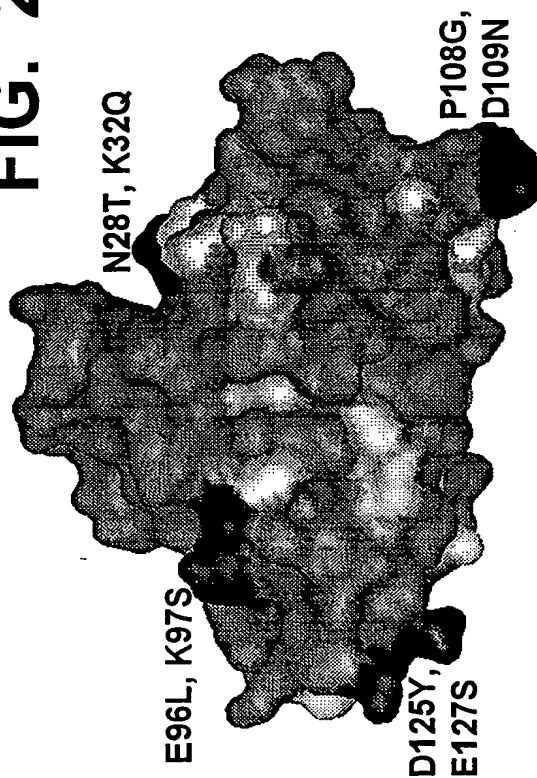
FIG. 24



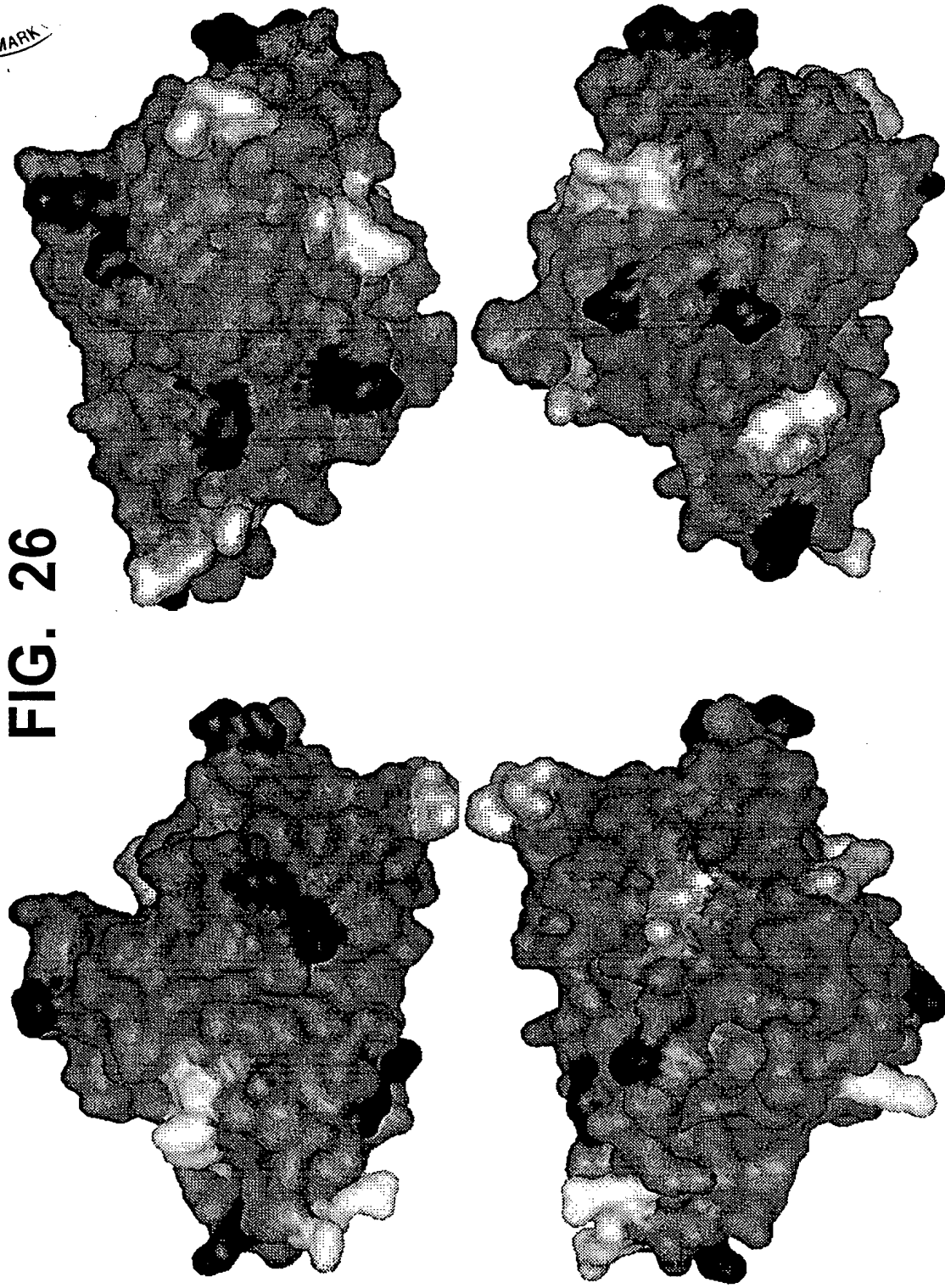
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FIG. 25



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**FIG. 26**

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FIG. 27

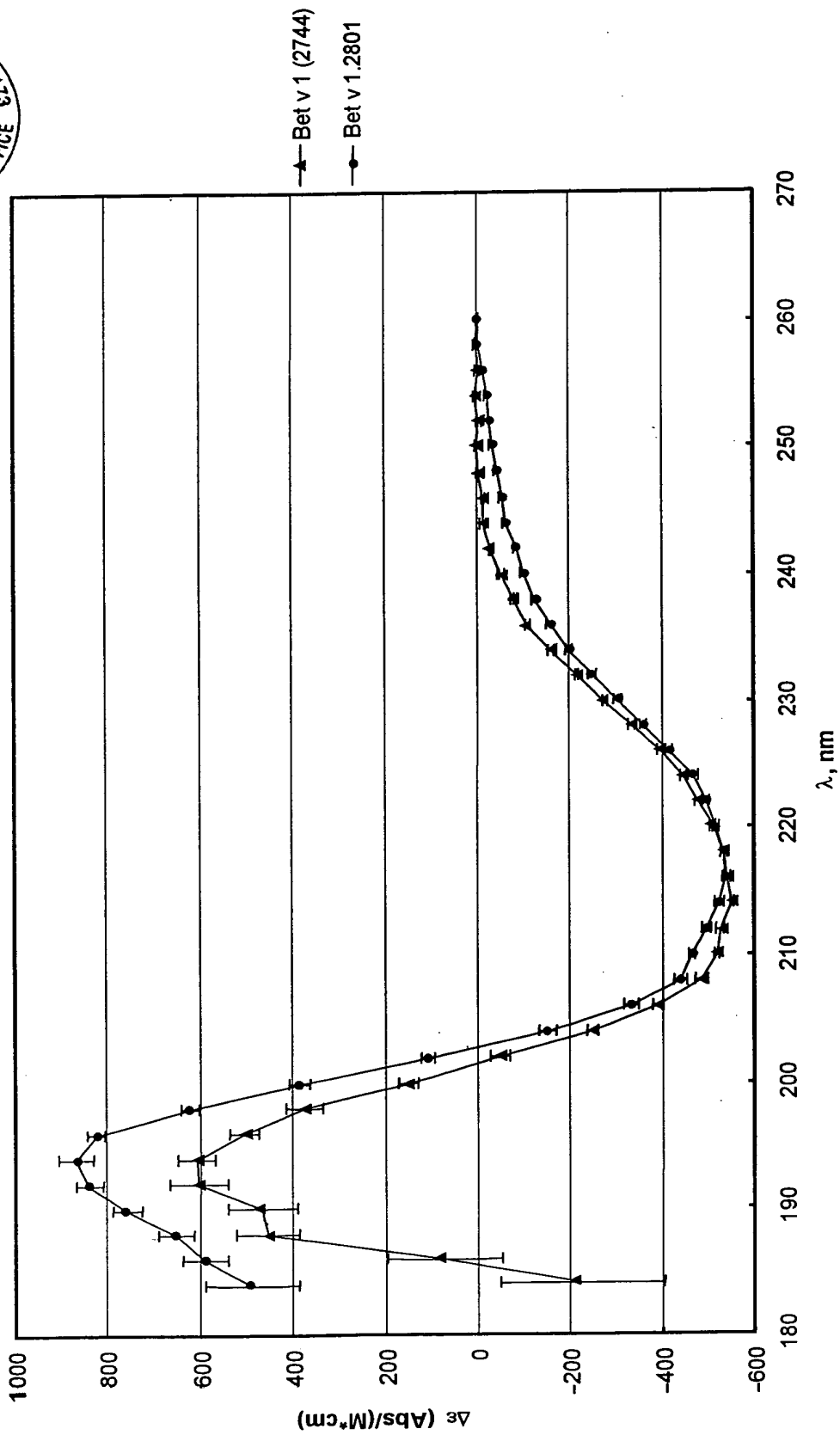
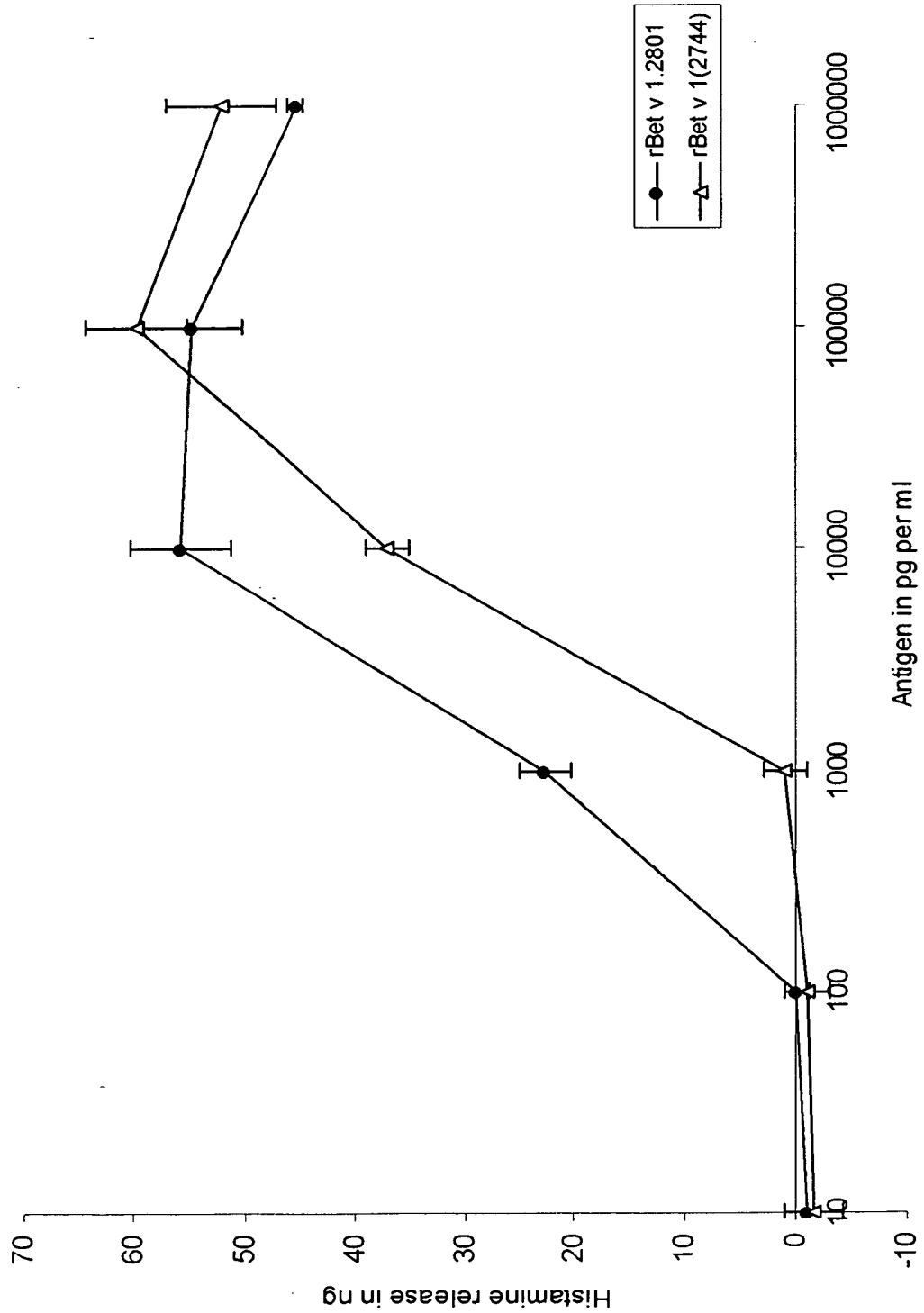




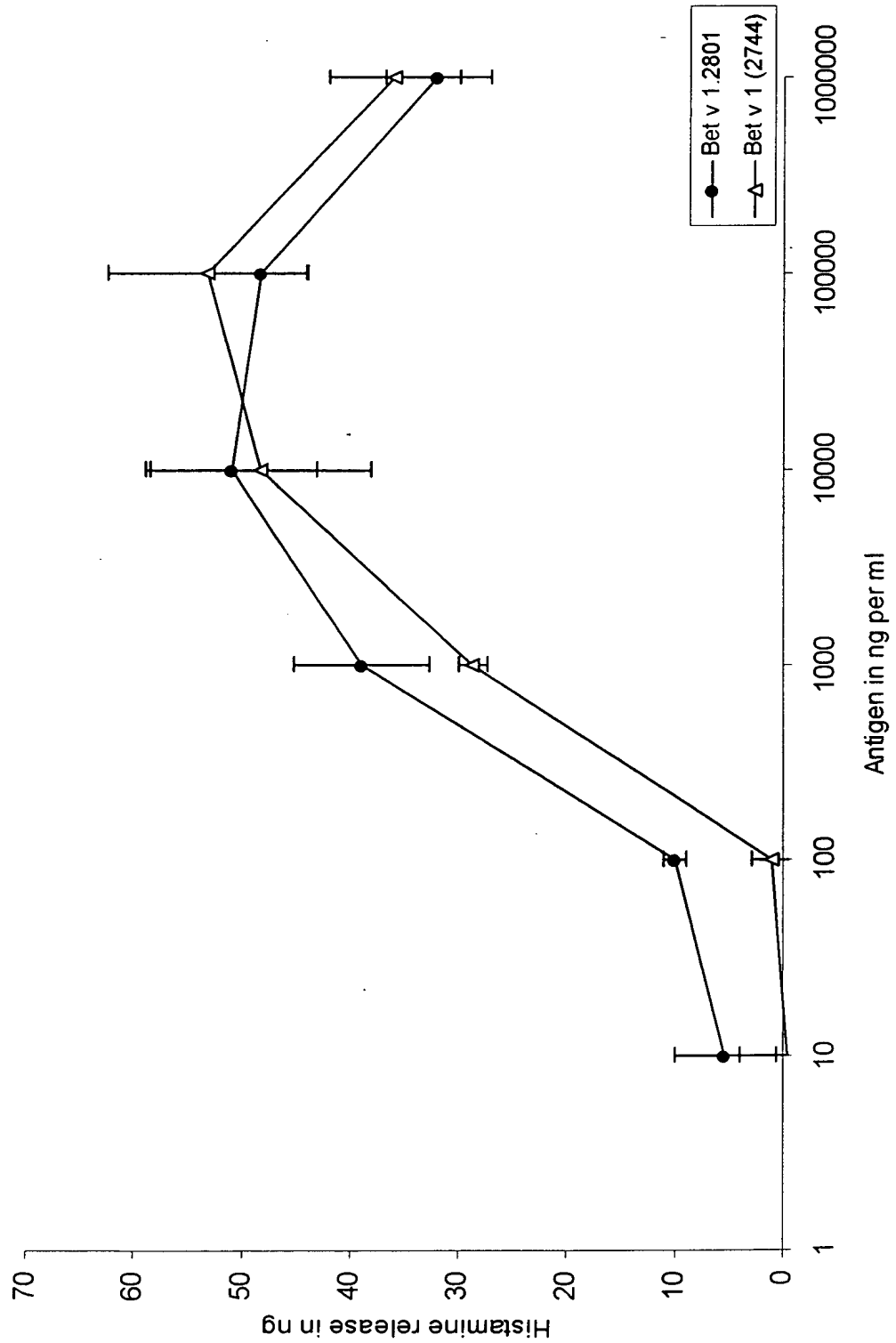
FIG. 28



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FIG. 29 A



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FIG. 29 B

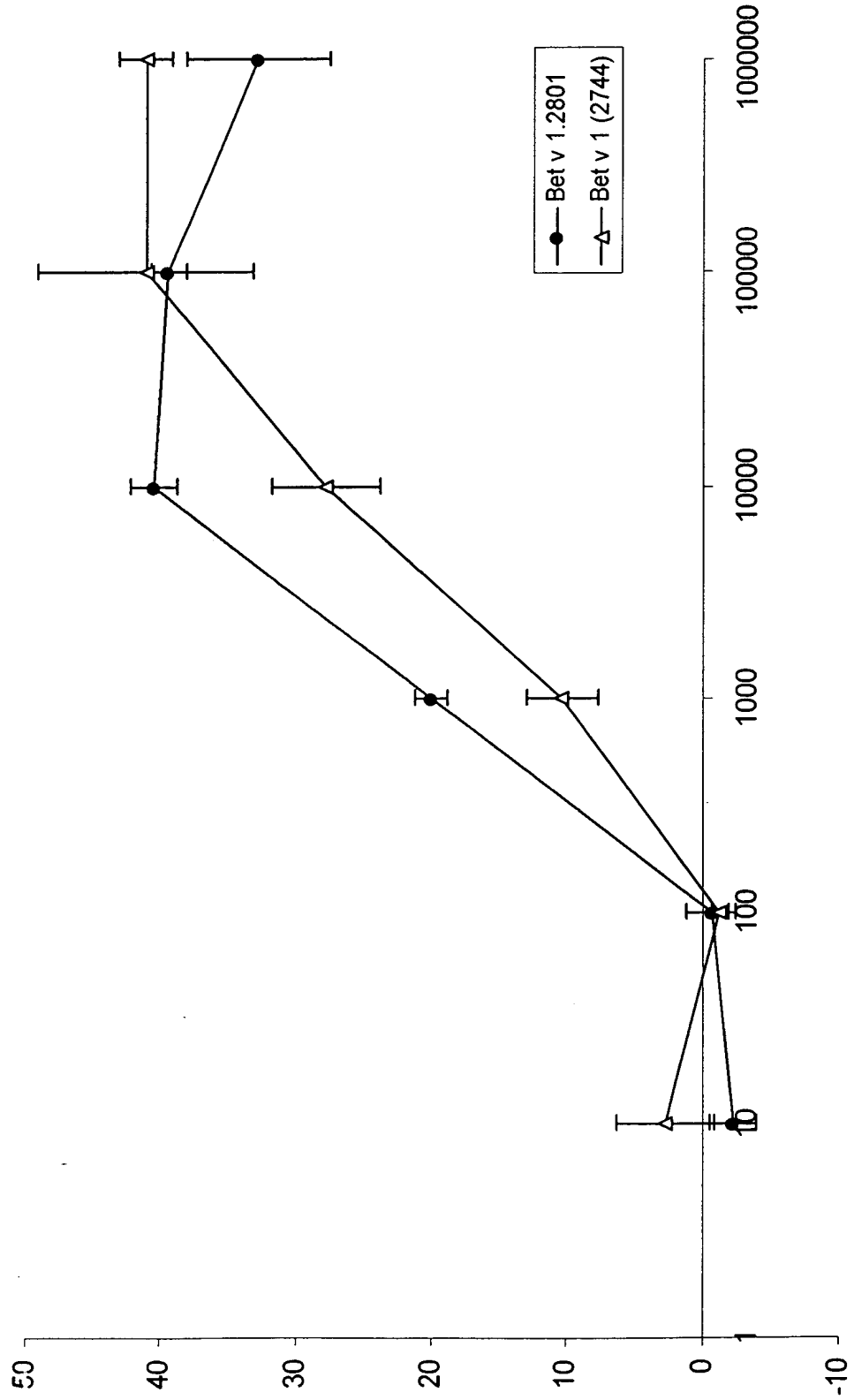
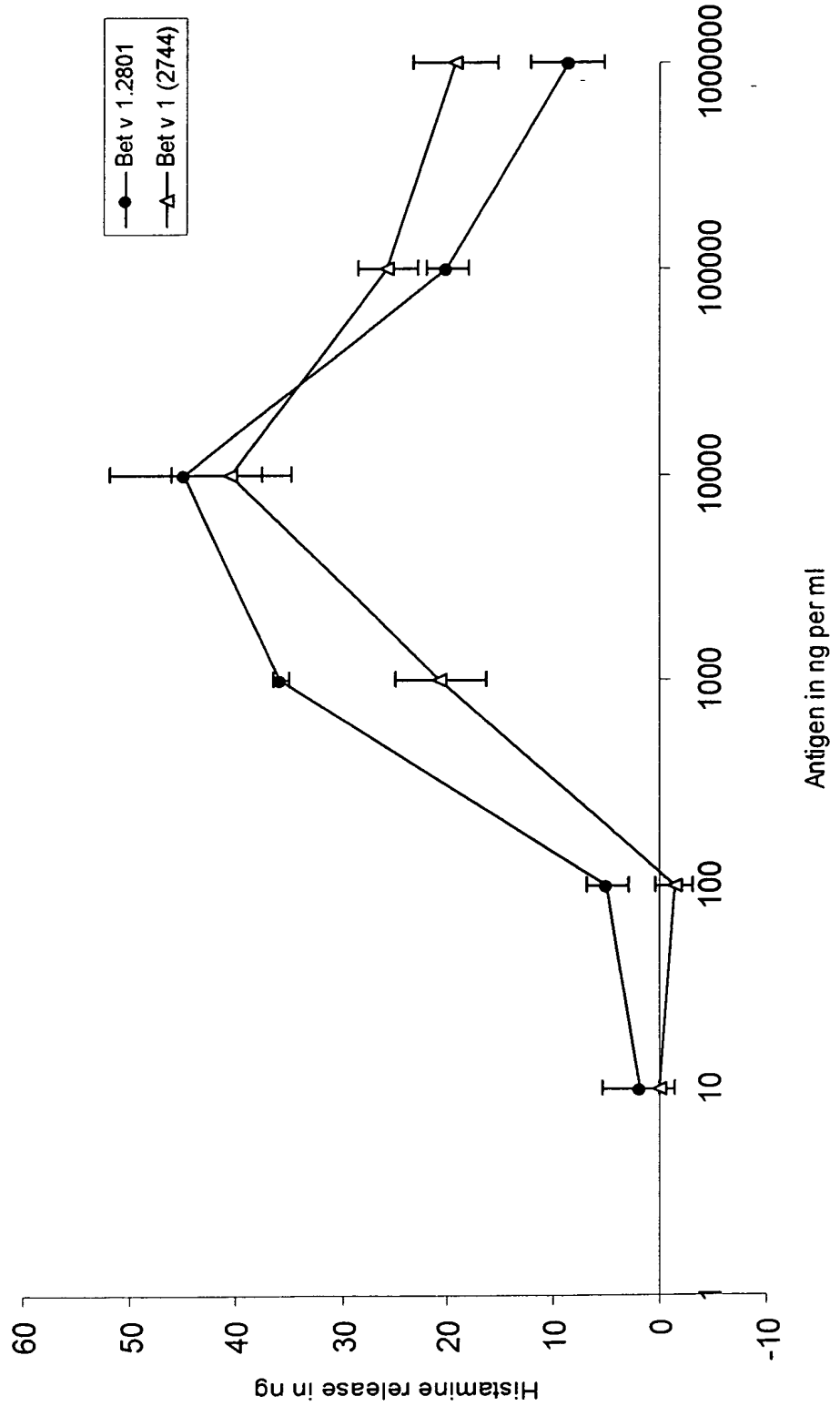




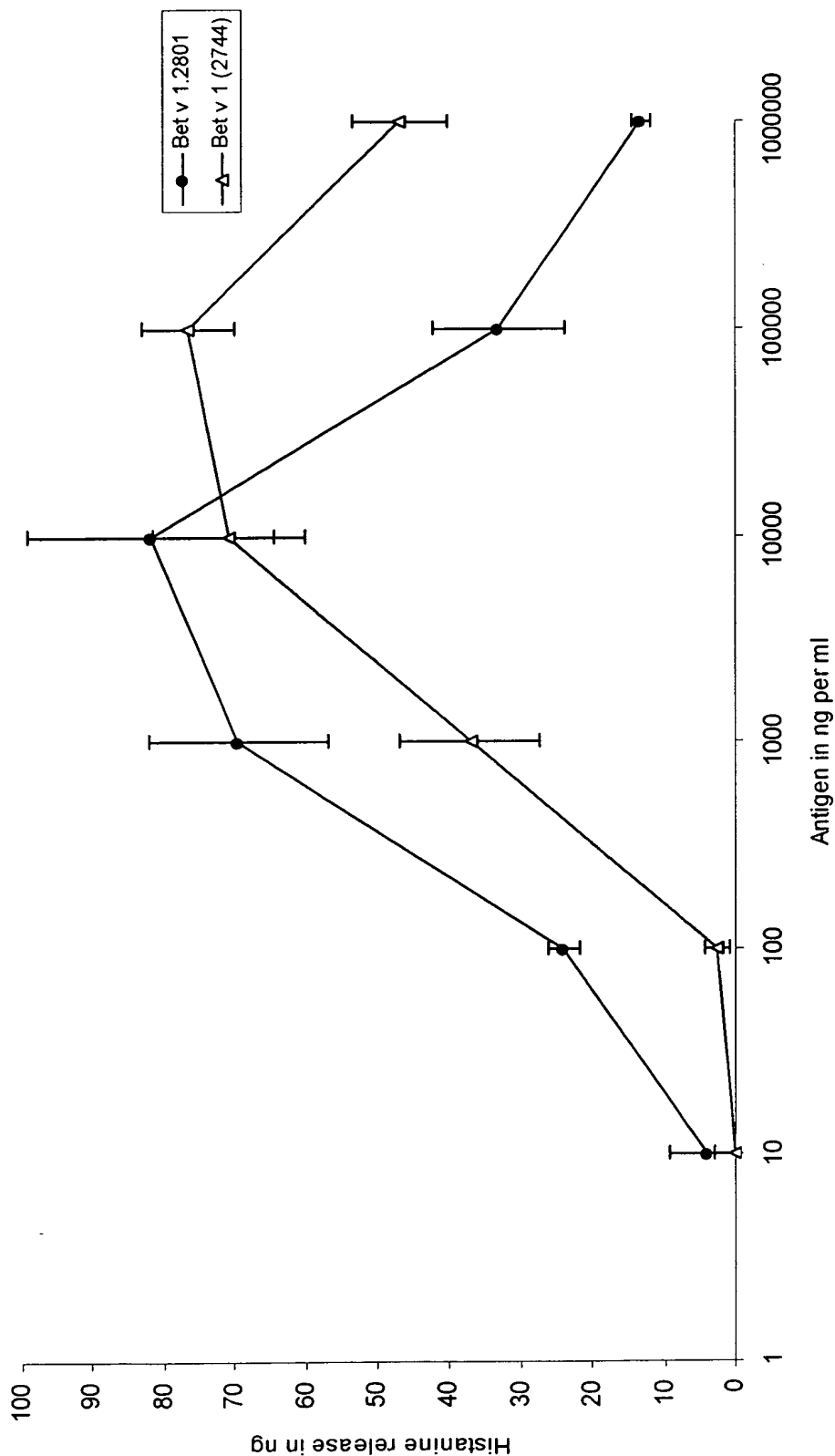
FIG. 29 C



10/001,245



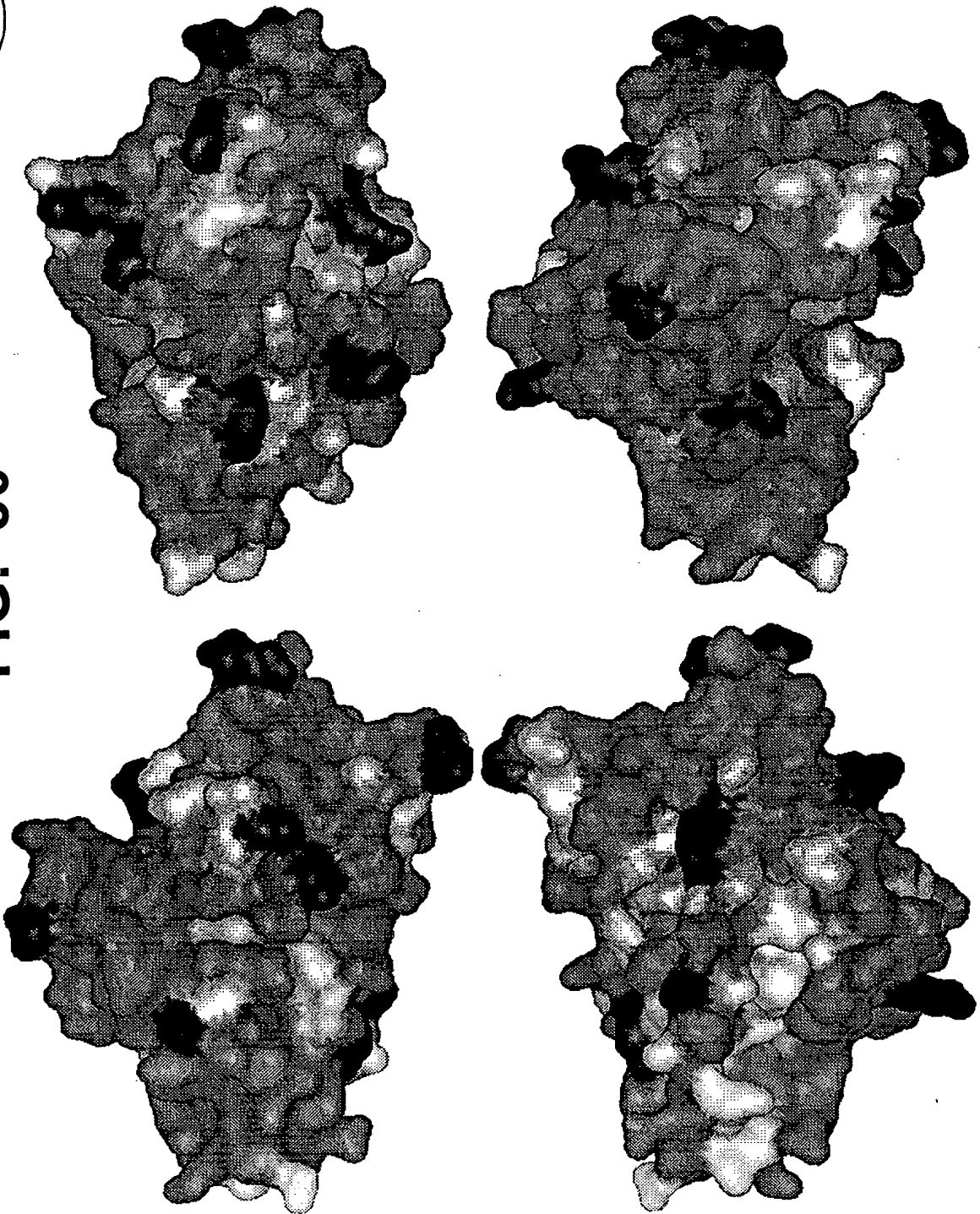
FIG. 29 D



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FIG. 30



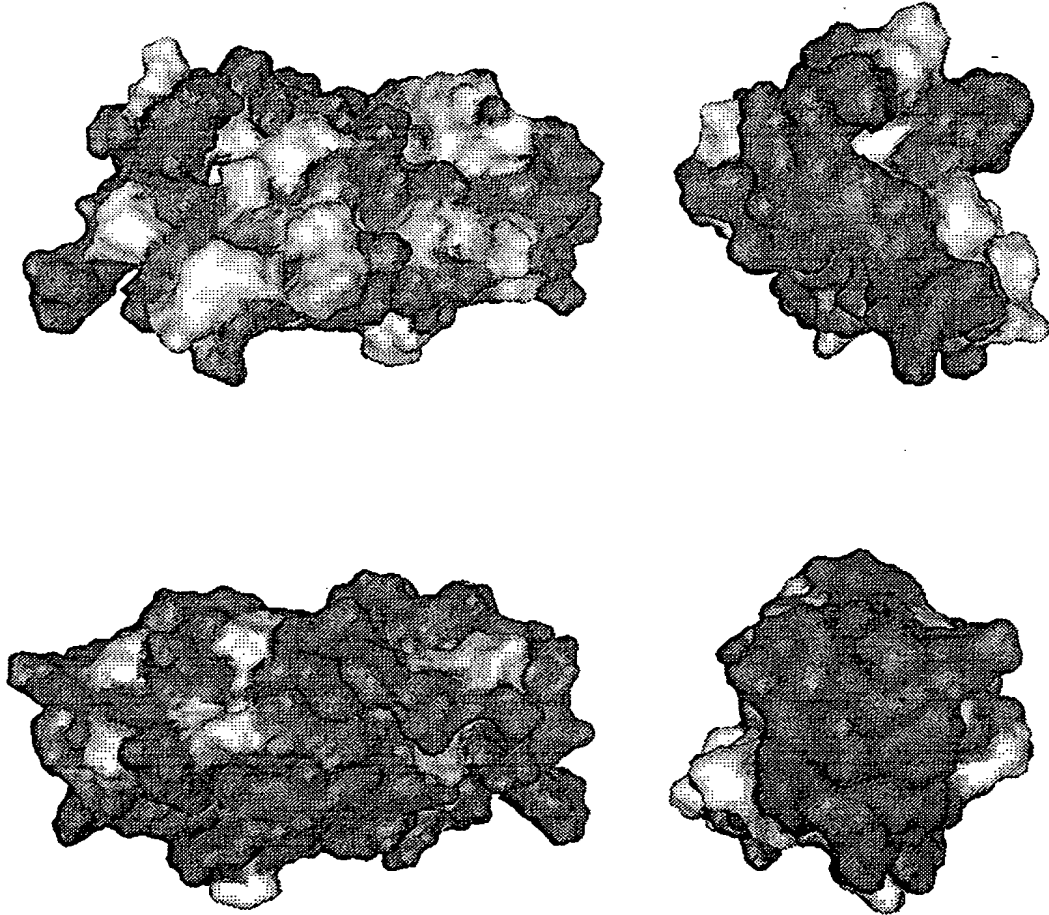
10/001,245



FIG. 31

K6A	sense	OB43	42-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCGCCGATTGTGCC- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
K15E	sense	OB44	67-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTGG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
H30N	sense	OB46	54-mer	5' -CGGGGTACCAGGATGTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTTATCAGTTGATGTTCCC- 3'
	anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC- 3'
H74N	sense	OB49	32-mer	5' -CATGGCATGCAATTACATGAAATGCCCATTTGG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
K82N	sense	OB50	50-mer	5' -CTACGCATGCCATTACATGAAATGCCCATTTGGTTAATGGACAA CAATATG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'

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**FIG. 33**

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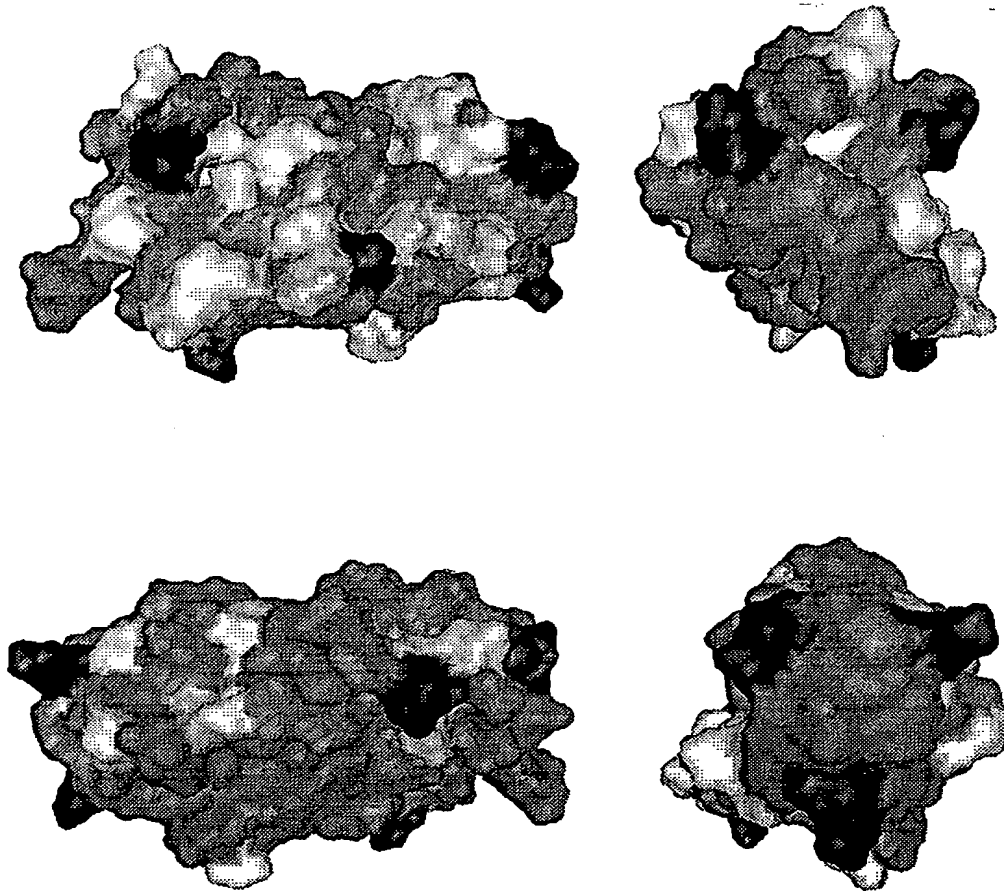
**FIG. 34**

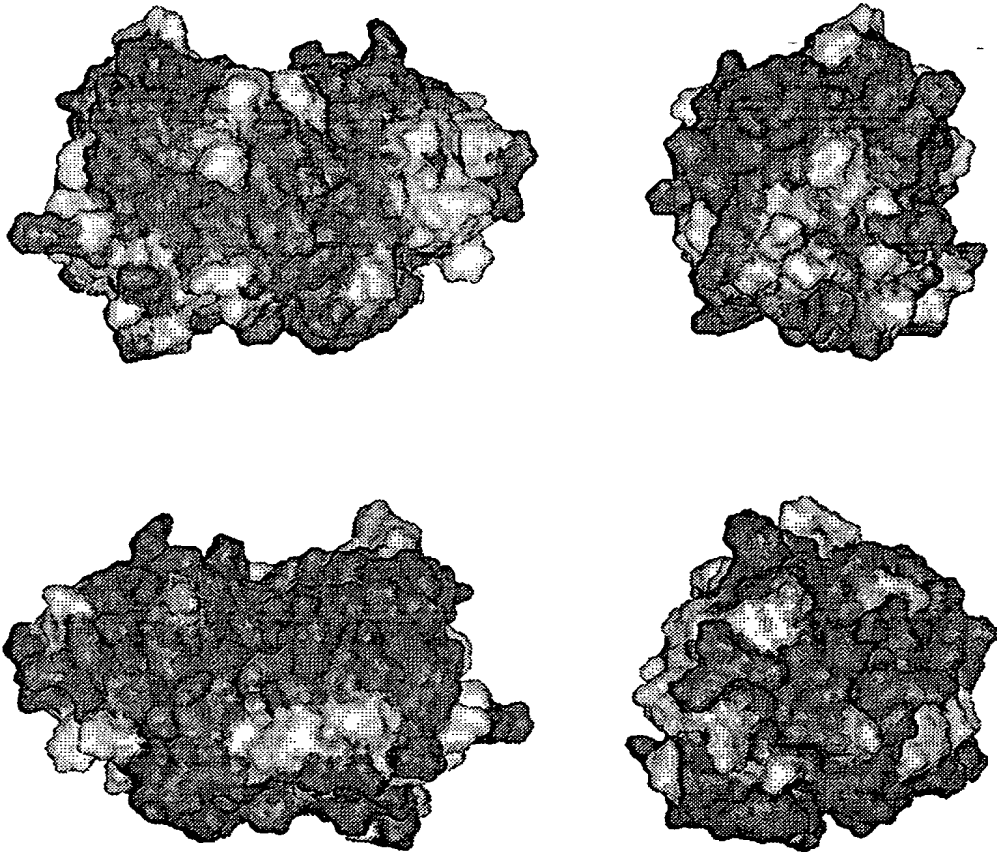


FIG. 35 A

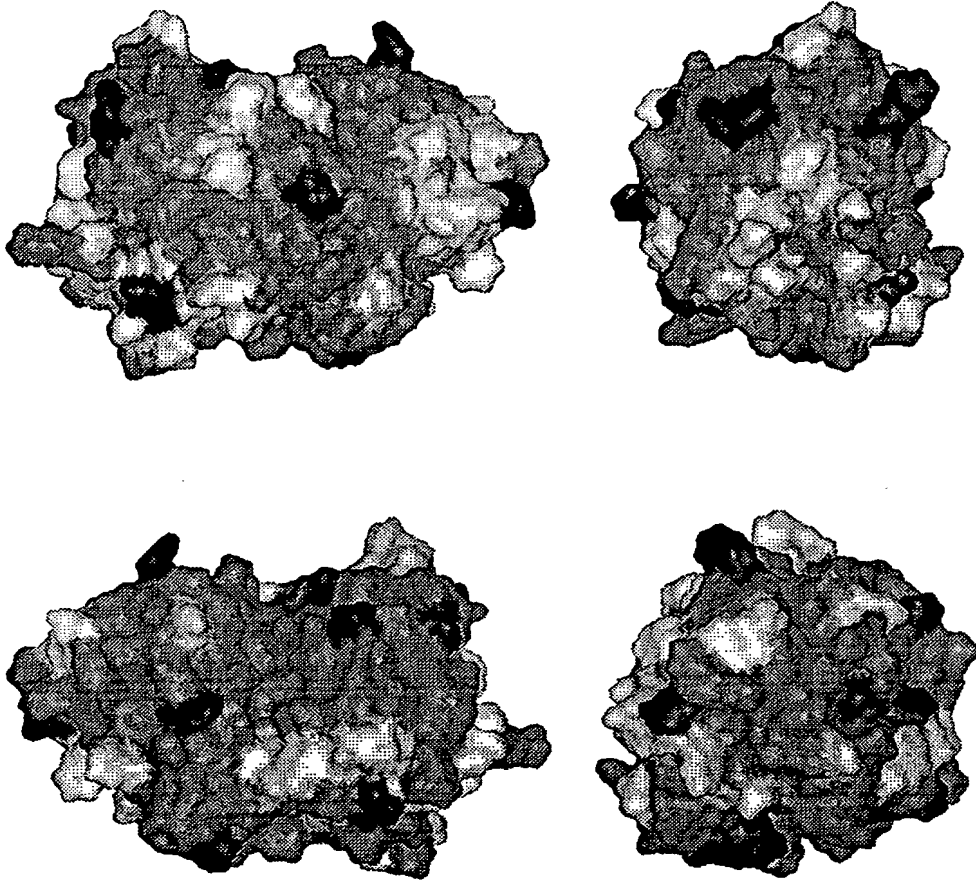
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	80	90	100	110	120	130
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Derp1	I P R G I E Y I Q H N G V V Q E S Y T R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V R K I R E A L A Q T H					
Eurm1.0101	I P R G I E Y I Q Q N G V V Q E H Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S M K I R Q A L T Q T H					
Eurm1.0102	I P R G I E Y I Q Q N G V V Q E H Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S M K I R Q A L T Q T H					
Derf1	I P R G I E Y I Q Q N G V V Q E H Y P Y V A R E Q R C R R P N A Q R Y G L K N Y C Q I S P P D V K K I R E A L T Q T H					
Eurm1	I P R G I E Y I Q Q N G V V Q E H Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S M K I R Q A L T Q T H					
Derf1	I P R G I E Y I Q Q N G V V E E R S Y P Y V A R E Q Q C R R P N A Q R Y G I S N Y C Q I Y P P D V K K I R E A L T Q T H					
	140	150	160	170	180	190
Derp1/ALK	S A I A V I I G I K D L D A F R H Y D G R T I I Q R D N G Y Q P N Y H A V N I V G Y S N A Q G V D Y W I V R R S W D T T					
Derp1	S A I A V I I G I K D L D A F R H Y D G R T I I Q R D N G Y Q P N Y H A V N I V G Y S N A Q G V D Y W I V R R S W D T T					
Eurm1.0101	T A V A V I I G I K D L N A F R H Y D G R T I I M Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R R S W D T T					
Eurm1.0101	T A V A V I I G I K D L N A F R H Y D G R T I I M Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R R S W D T T					
Eurm1.0102	T A V A V I I G I K D L N A F R H Y D G R T I I M Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R R S W D T T					
Derf1	T A I A V I I G I K D L R A F Q H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G S T Q G D D Y W I V R R S W D T T					
Eurm1	T A V A V I I G I K D L N A F R H Y D G R T I I M Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R R S W D T T					
Derf1	T A I A V I I G I K D L R A F Q H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G S T Q G V D Y W I V R R S W D T T					
	200	210	220			
Derp1/ALK	W G D N G Y G Y F F A A N I D L M M I E E Y P Y V V I L					
Derp1	W G D N G Y G Y F F A A N I D L M M I E E Y P Y V V I L					
Eurm1.0101	W G D N G Y G Y F F A A N I N L M M I E E Q Y P Y V V M L					
Eurm1.0101	W G D N G Y G Y F F A A N I N L M M I E E Q Y P Y V V M L					
Eurm1.0102	W G D N G Y G Y F F A A N I N L M M I E E Q Y P Y V V I L					
Derf1	W G D S G Y G Y F F A G N N I L M M I E E Q Y P Y V V I M					
Eurm1	W G D N G Y G Y F F A A N I N L					
Derf1	W G D S G Y G Y F F A G N N I L					

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**FIG. 36**

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**FIG. 37**

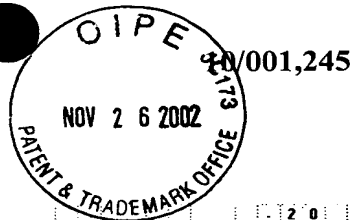
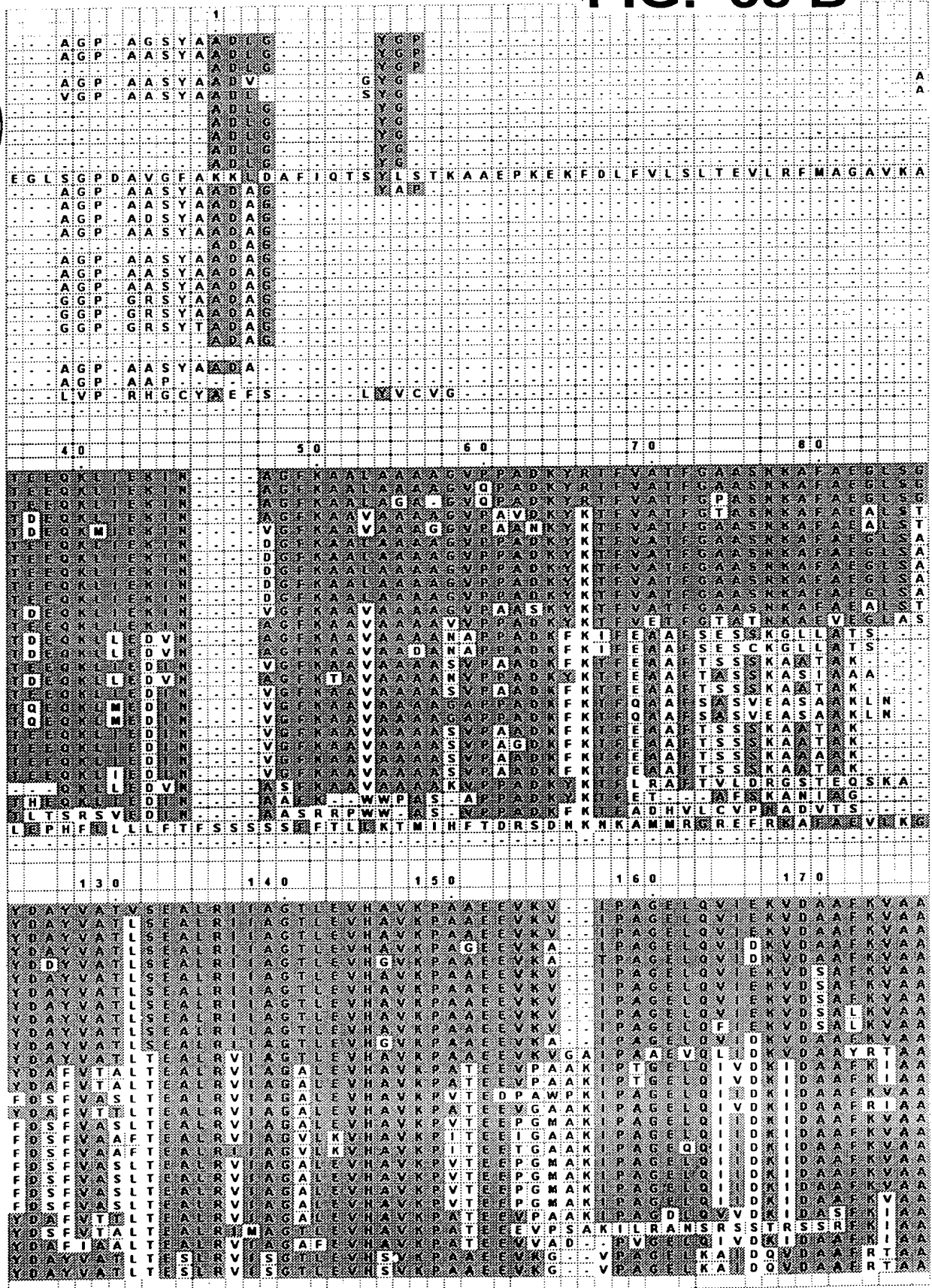


FIG. 38 A

			2 0	1 0	
trj081341j081341	Phl p 5.0103		MAVHQYTVALFLAVALV		
trj040960j040960	Phl p 5		MAVHQYTVALFLAVALV		
spj040962jMP5A_PHLPR	Phl p 5 A		MAVHQYTVALFLAVALV		
spjP22266jMP92_POAPR	Poa p 5 (KBG41)		MAVHQYTVALFLAVALV		
spjP22266jMP93_POAPR	Poa p 5 (KBG60)		MAVQKYTVALFLAVALV		
trj065319j065319	Phl p 5				
trj065320j065320	Phl p 5				
trj065321j065321	Phl p 5				
trj065318j065318	Phl p 5				
trjP93467jP93467	Phl p 5				
spjP22284jMP91_POAPR	Poa p 5 (KBG 31)		MDKANGAYKTALKAA SAVAPAEKFPVFOATFDKNLK		
spj040237jMP5B_LOLPR	Lol p 5B		MAVQKHTVALFLAVALV		
trj09XF24j09XF24	Lol p 5A		MAVQKHTVALFLAVALV		
trj09SC99j09SC99	Lol p 5C		MAVQKHTVALFLAVALV		
trj081343j081343	Phl p 5.0206		MAVQKHTVALFLAVALV		
trj023972j023972	Hol 15				
trj081344j081344	Phl p 5.0207		MAVQKHTVALFLAVALV		
trjAAG42255jAAG42255	Hol 15B		MAVQKHTVALFLAVALV		
trjAAG42254jAAG42254	Poa p 5		MAVQKHTVALFLAVALV		
trj081342j081342	Phl p 5.0203	SVKRSNGSAEVH	RGAVPRRGPR		
trjP93466jP93466	Phl p 5		AVPRRGPR		
spj040963jMP5B_PHLPR	Phl p 5B		AAA AVPRRGPR		
trj09SBE0j09SBE0	Phl p 5.0204				
trj023971j023971	Phl p 5.02				
spjP56166jMP53_PHAHQ	Pha a 5.3		MAVQKHTVALFLAVALV		
HAAQ	Pha a 5.1		MAVQKHTVALFLAVALV		
trj004828j004828	Hor v 9		MA NSGREHS AVPRRRNLVA		
trjQ39995jQ39995	Hor v 5 (30kDa)				
		1 0	2 0	3 0	
trj081341j081341	Phl p 5.0103		ATPAAAPAGYTPATPAAPAG		AEPAAGKAT
trj040960j040960	Phl p 5		ATPAAAPAGYTPATPAAPAG		ADAAGKAT
spj040962jMP5A_PHLPR	Phl p 5 A		ATPAAAPAGYTPATPAAPAG		AAAGKAT
spjP22266jMP92_POAPR	Poa p 5 (KBG41)	PATL	ATPAAAPAGYTPATPAAPAG		AAAGKAT
spjP22266jMP93_POAPR	Poa p 5 (KBG60)	P	ATPAAAPAGYTPATPAAPAG		AAAGKAT
trj065319j065319	Phl p 5		GPATPAAPAG		AAAGKAT
trj065320j065320	Phl p 5		GPATPAAPAG		AAAGKAT
trj065321j065321	Phl p 5		GPATPAAPAG		AAAGKAT
trj065318j065318	Phl p 5		GPATPAAPAG		AAAGKAT
trjP93467jP93467	Phl p 5		GPATPAAPAG		AAAGKAT
spjP22284jMP91_POAPR	Poa p 5 (KBG 31)	PPASKFPKAPKPVAAAT	TPATPAAPAG		AAAGKAT
spj040237jMP5B_LOLPR	Lol p 5B	ATP	TPATPAAPAG		AAAGKAT
trj09XF24j09XF24	Lol p 5A		TPATPAAPAG		AAAGKAT
trj09SC99j09SC99	Lol p 5C		TPATPAAPAG		AAAGKAT
trj081343j081343	Phl p 5.0206		TPATPAAPAG		AAAGKAT
trj023972j023972	Hol 15		TPATPAAPAG		AAAGKAT
trj081344j081344	Phl p 5.0207		TPATPAAPAG		AAAGKAT
trjAAG42255jAAG42255	Hol 15B		TPATPAAPAG		AAAGKAT
trjAAG42254jAAG42254	Poa p 5		TPATPAAPAG		AAAGKAT
trj081342j081342	Phl p 5.0203		TPATPAAPAG		AAAGKAT
trjP93466jP93466	Phl p 5		TPATPAAPAG		AAAGKAT
spj040963jMP5B_PHLPR	Phl p 5B		TPATPAAPAG		AAAGKAT
trj09SBE0j09SBE0	Phl p 5.0204		TPATPAAPAG		AAAGKAT
trj023971j023971	Phl p 5.02		TPATPAAPAG		AAAGKAT
spjP56166jMP53_PHAHQ	Pha a 5.3		TPATPAAPAG		AAAGKAT
HAAQ	Pha a 5.1		TPATPAAPAG		AAAGKAT
trj004828j004828	Hor v 9		TPATPAAPAG		AAAGKAT
trjQ39995jQ39995	Hor v 5 (30kDa)		TPATPAAPAG		AAAGKAT
		9 0	1 0 0	1 1 0	1 2 0
trj081341j081341	Phl p 5.0103	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj040960j040960	Phl p 5	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
spj040962jMP5A_PHLPR	Phl p 5 A	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
spjP22266jMP92_POAPR	Poa p 5 (KBG41)	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
spjP22266jMP93_POAPR	Poa p 5 (KBG60)	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj065319j065319	Phl p 5	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj065320j065320	Phl p 5	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj065321j065321	Phl p 5	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj065318j065318	Phl p 5	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trjP93467jP93467	Phl p 5	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
spjP22284jMP91_POAPR	Poa p 5 (KBG 31)	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
spj040237jMP5B_LOLPR	Lol p 5B	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj09XF24j09XF24	Lol p 5A	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj09SC99j09SC99	Lol p 5C	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj081343j081343	Phl p 5.0206	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj023972j023972	Hol 15	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj081344j081344	Phl p 5.0207	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trjAAG42255jAAG42255	Hol 15B	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trjAAG42254jAAG42254	Poa p 5	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj081342j081342	Phl p 5.0203	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trjP93466jP93466	Phl p 5	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
spj040963jMP5B_PHLPR	Phl p 5B	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj09SBE0j09SBE0	Phl p 5.0204	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj023971j023971	Phl p 5.02	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
spjP56166jMP53_PHAHQ	Pha a 5.3	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
HAAQ	Pha a 5.1	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trj004828j004828	Hor v 9	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		
trjQ39995jQ39995	Hor v 5 (30kDa)	EPKKG	AAATSSSKAALTSKLDAAAYKLAAYKYTAEGGATPEAKK		

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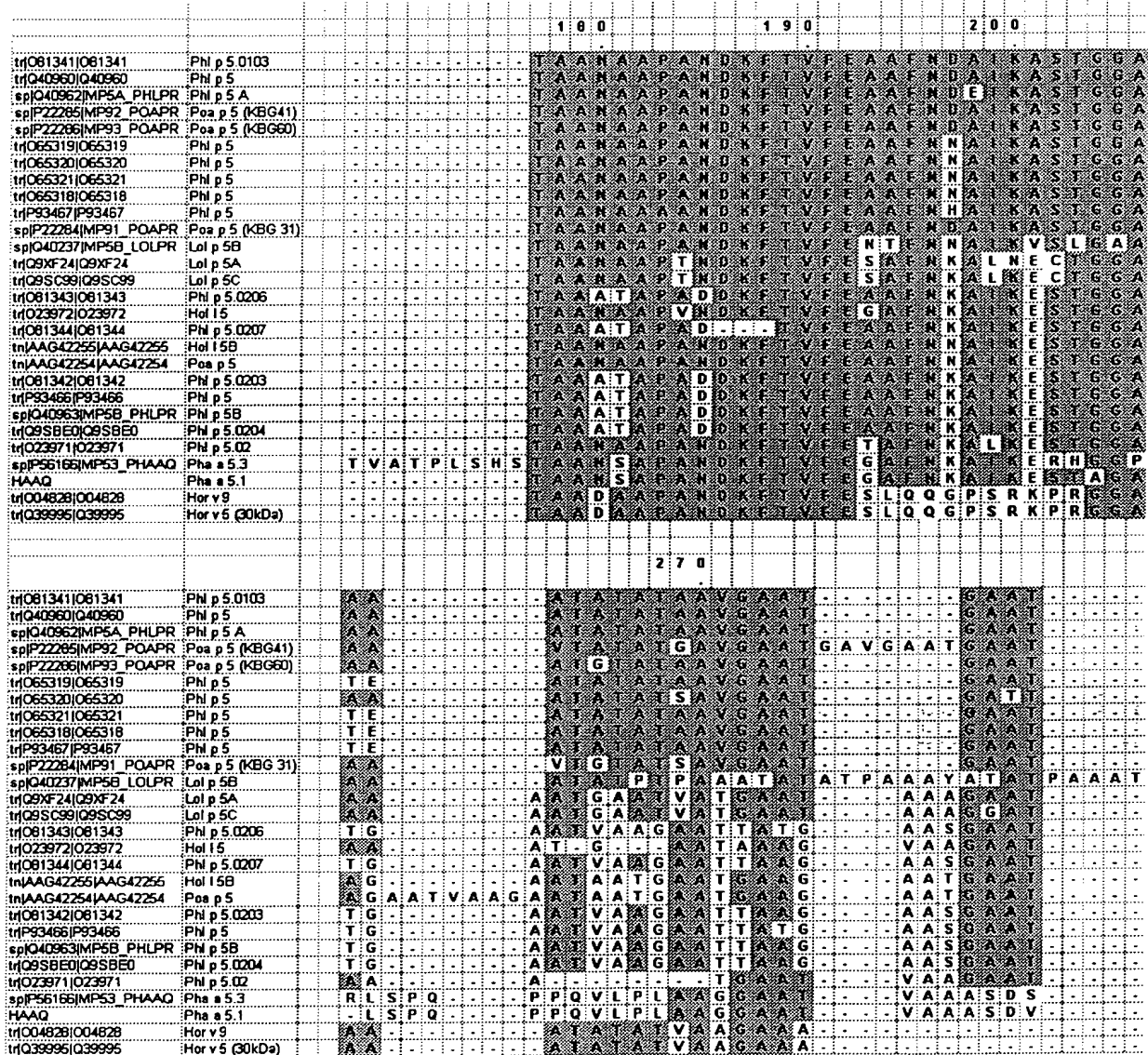
FIG. 38 B

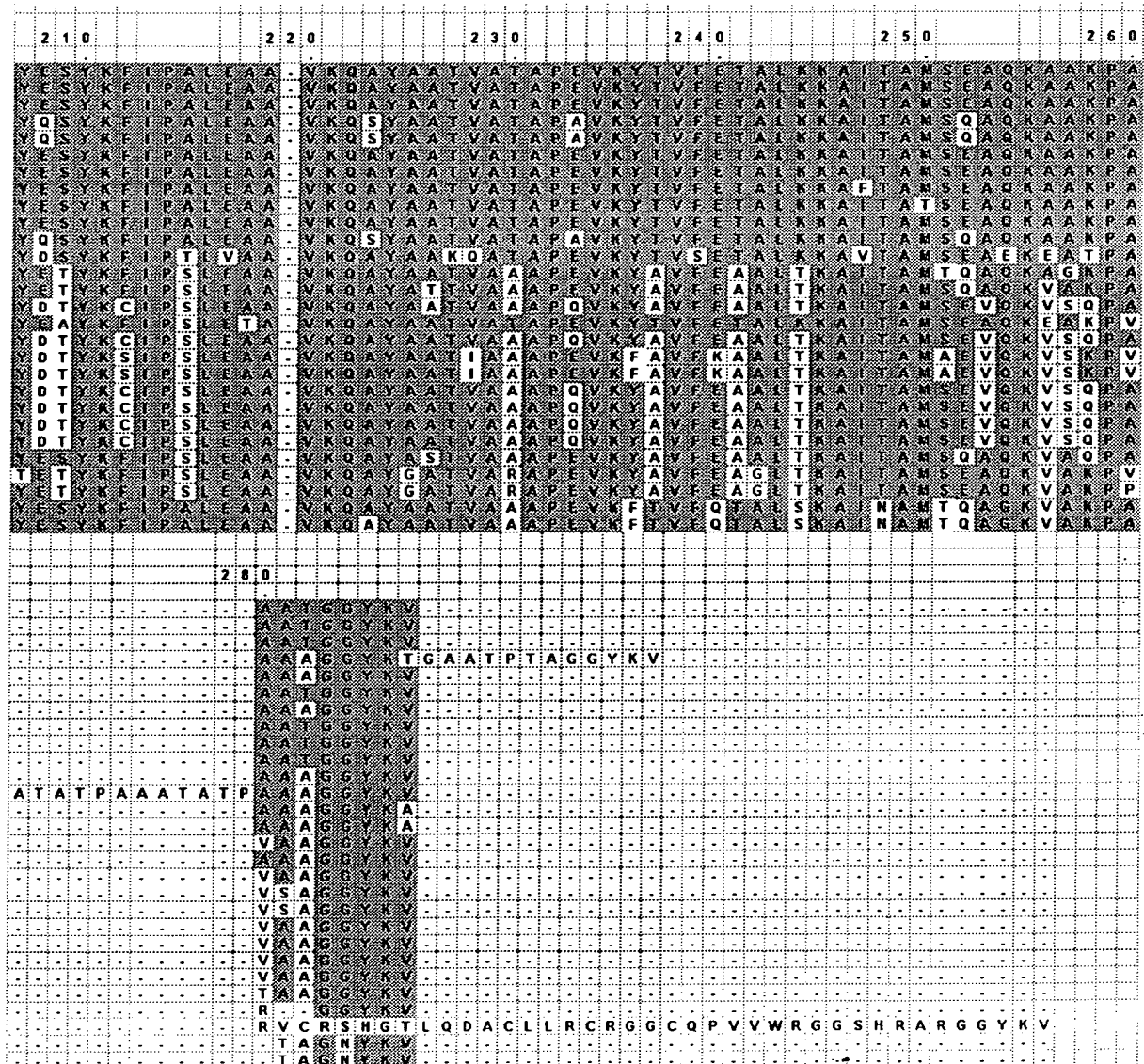


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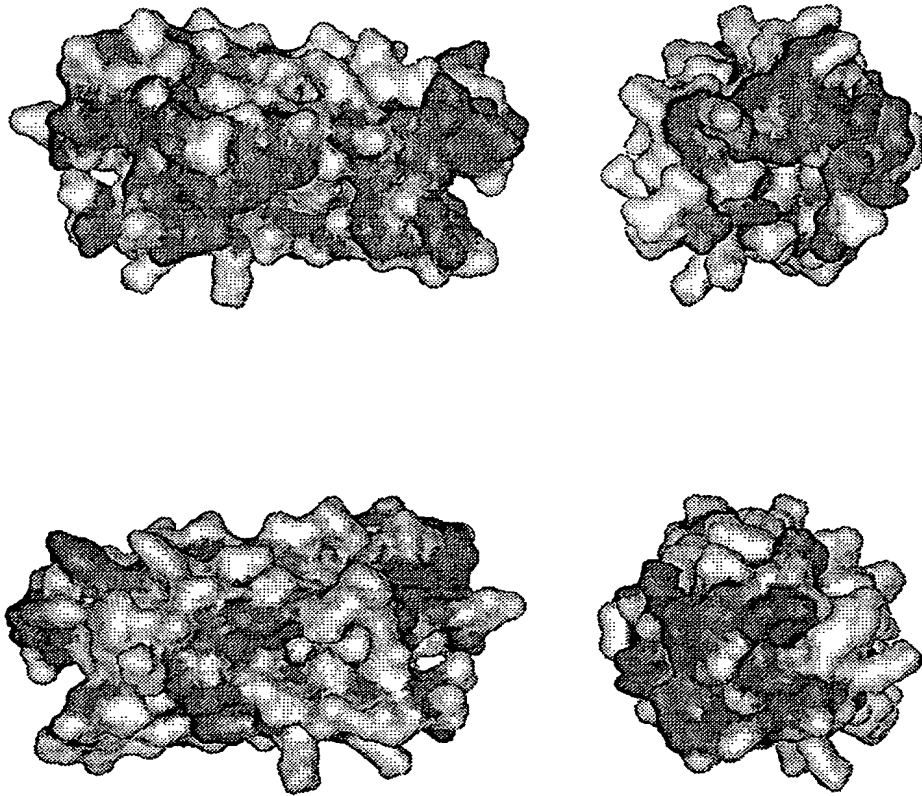


FIG. 38 C

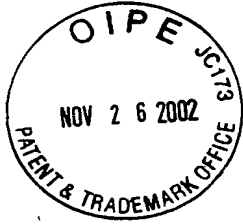
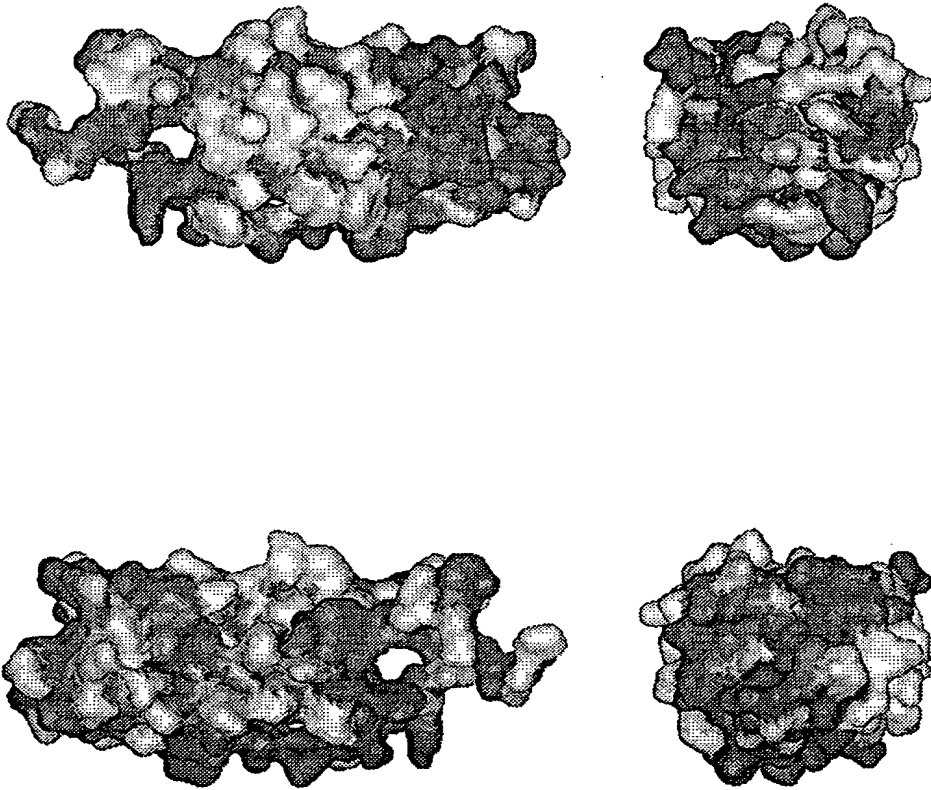




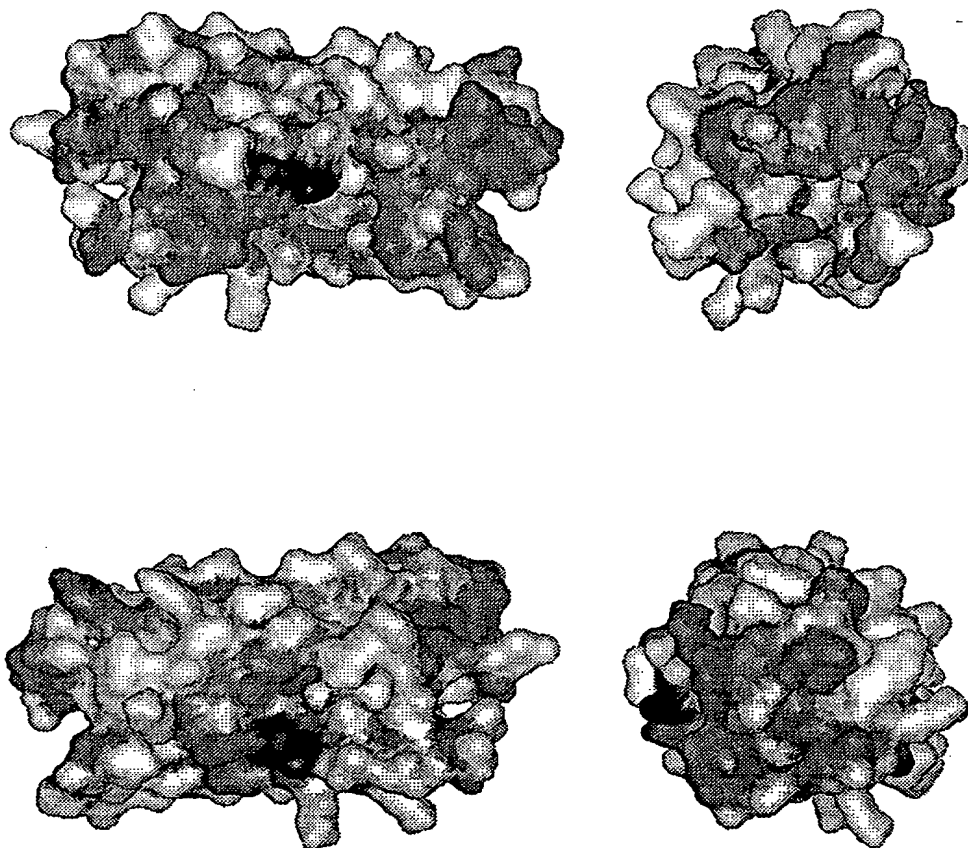
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**FIG. 39 A**

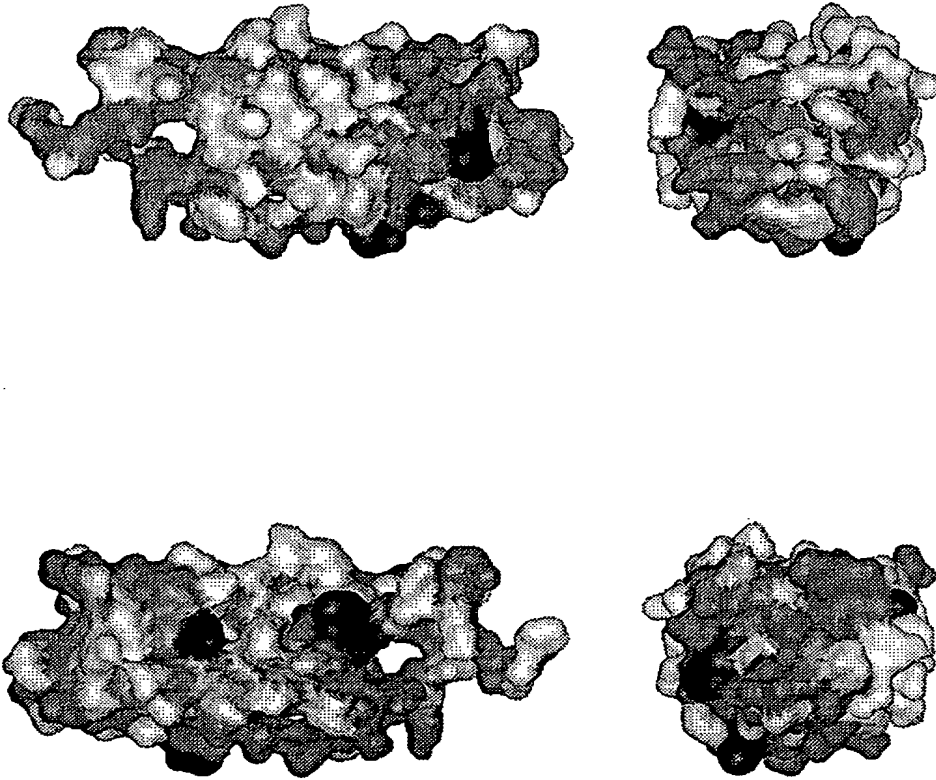
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**FIG. 39 B**

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**FIG. 40 A**

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**FIG. 40 B**

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FIG. 41

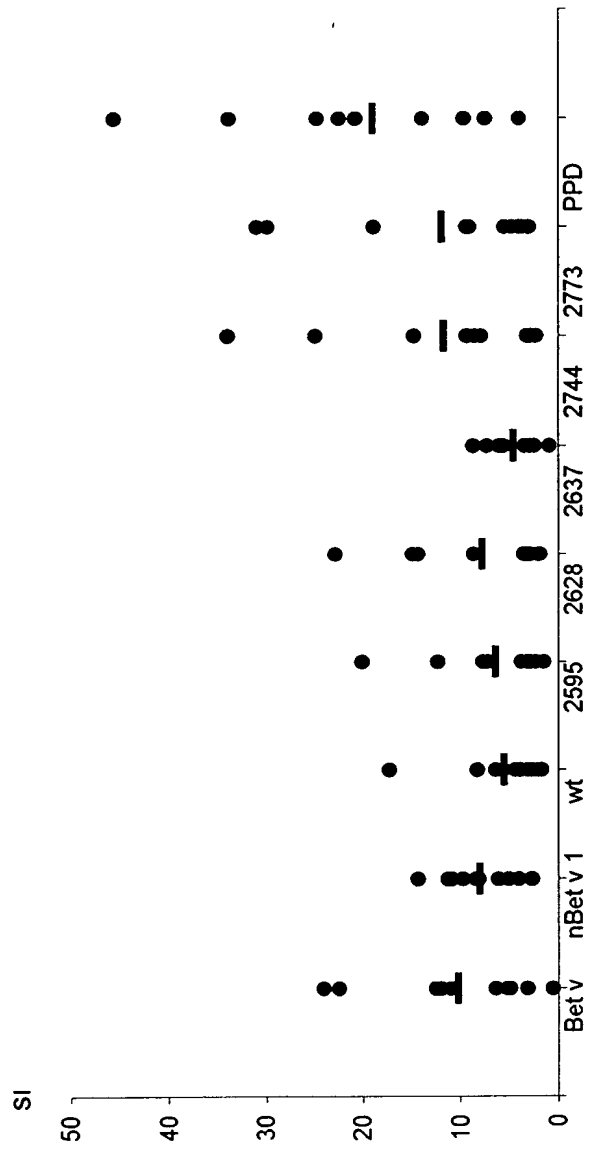
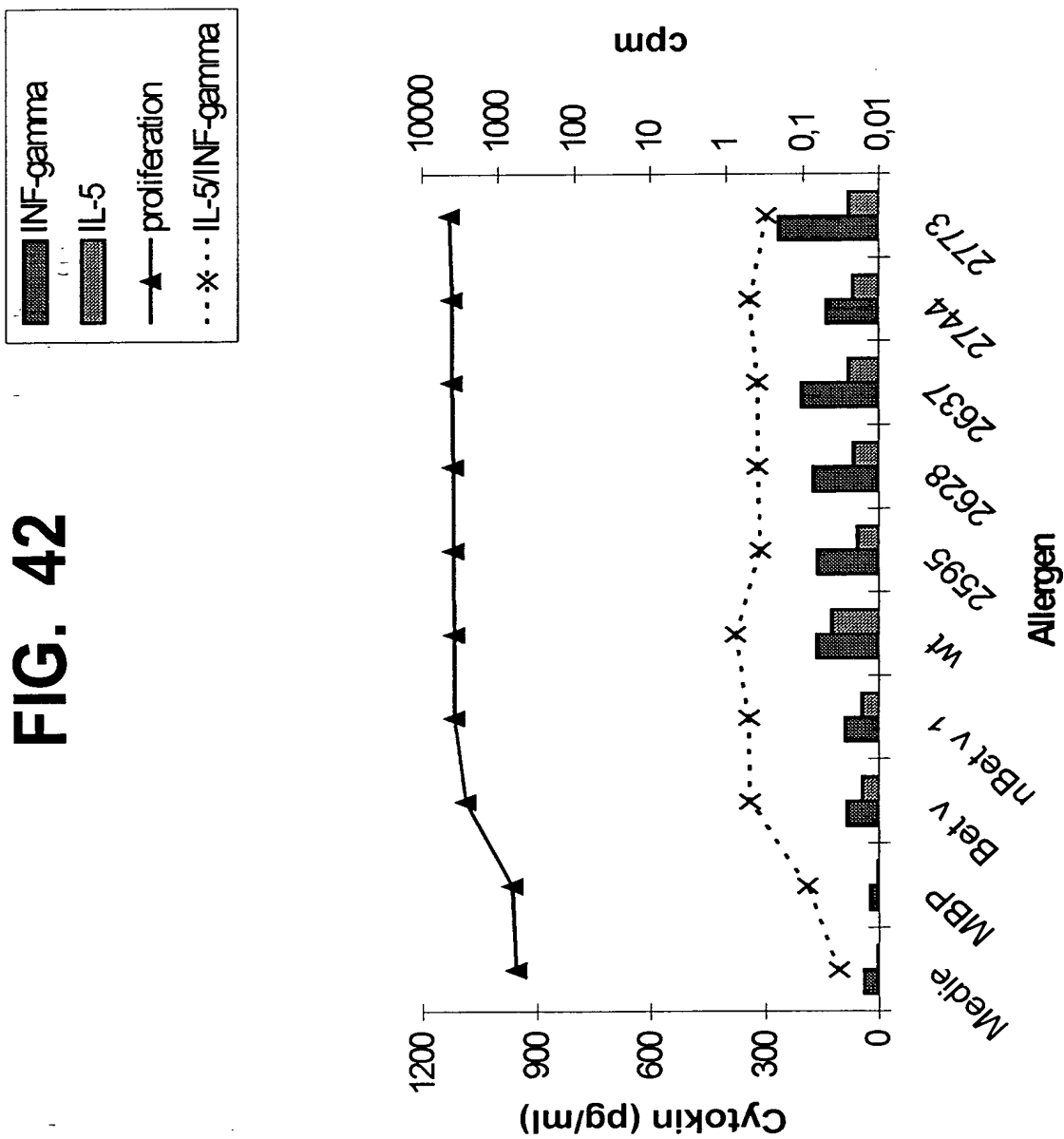




FIG. 42



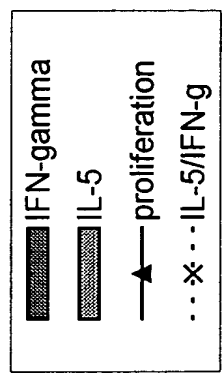


FIG. 43

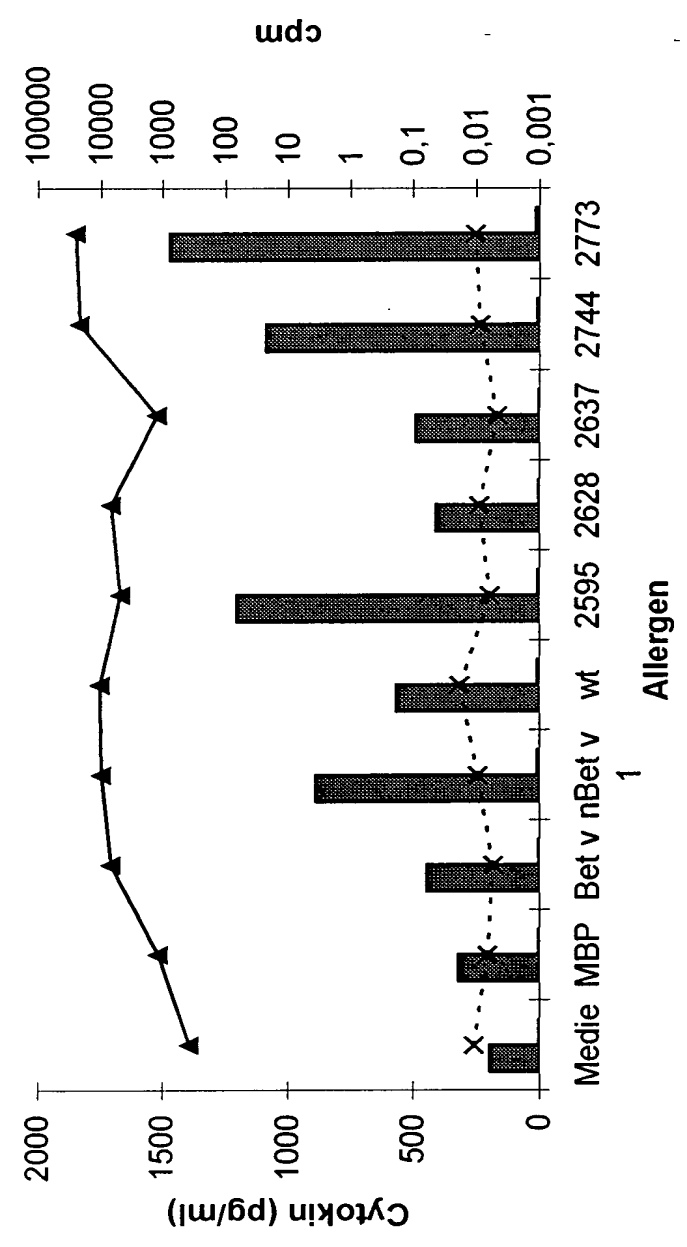




FIG. 44

